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Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

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Other Formats: Links: ☐ Order this document*Oncogene* 1999 Jan 14;18(2):559-64

A tumor specific single chain antibody dependent gene expression system.

Mary MN, Venot C, Caron de Fromentel C, Debussche L, Conseiller E, Cochet O, Gruel N, Teillaud JL, Schweighoffer F, Tocque B, Bracco L

Gene Medicine Department, Rhone-Poulenc Rorer S.A., Vitry-sur-Seine, France.

The design of conditional gene expression systems restricted to given tissues or cellular types is an important issue of gene therapy. Systems based on the targeting of molecules characteristic of the pathological state of tissues would be of interest. We have developed a synthetic transcription factor by fusing a single chain antibody (scFv) directed against p53 with the bacterial tetracycline repressor as a DNA binding domain. This hybrid protein binds to p53 and can interact with a synthetic promoter containing tetracycline-operator sequences. Gene expression can now be specifically achieved in tumor cells harboring an endogenous mutant p53 but not in a wild-type p53 containing tumor cell line or in a non-transformed cell line. Thus, a functional transactivator centered on single chain antibodies can be expressed intracellularly and induce gene expression in a scFv-mediated specific manner. This novel class of transcriptional transactivators could be referred as 'trabodies' for transcription-activating-antibodies. The trabodies technology could be useful to any cell type in which a disease related protein could be the target of specific antibodies.

PMID: 9927213, UI: 99124403

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Oncogene 1999 Jan 14;18(2):551-7

Restoration of transcriptional activity of p53 mutants in human tumour cells by intracellular expression of anti-p53 single chain Fv fragments.

Caron de Fromental C, Gruel N, Venot C, Debussche L, Conseiller E, Dureuil C, Teillaud JL, Tocque B, Bracco L

Gene Medicine Department, Rhone-Poulenc Rorer SA, Vitry sur Seine, France.

We report here the production and the properties of single chain Fv fragments (scFvs) derived from the anti-p53 monoclonal antibodies PAb421 and 11D3. 11D3 is a newly generated monoclonal antibody which exhibits properties very comparable to those of PAb421. The scFvs PAb421 and 11D3 are able to stably associate with p53 and to restore the DNA binding activity of some p53 mutants in vitro. When expressed in p53 -/- human tumour cells, the scFv421 is essentially localized in the cytoplasm in the absence of p53, and in the nucleus when exogenous p53 is present. Thus, p53 is also able to stably associate with an anti-p53 scFv in cells. Cotransfection of p53 -/- human tumour cells with expression vectors encoding the His273 p53 mutant and either scFv leads to restoration of the p53 mutant deficient transcriptional activity. These data demonstrate that, in human tumour cells, these scFvs are able to restore a function essential for the tumour suppressor activity of p53 and may represent a novel class of molecules for p53-based cancer therapy.

PMID: 9927212, UI: 99124402

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Other Formats: Links: ☐ Order this document*Biochem Biophys Res Commun* 1997 Jan 13;230(2):242-6

Characterization of scFv-421, a single-chain antibody targeted to p53.

Jannot CB, Hynes NE

Friedrich Miescher Institute, Basel, Switzerland.

A gene encoding a single-chain antibody (scFv) which specifically binds the tumor suppressor protein p53 has been constructed from RNA of hybridoma cells producing Pab 421. scFv-421 which was expressed and purified from bacteria specifically binds p53. scFv-421, as well as the previously described scFv-FRP5 and -R1R (1), were expressed intracellularly in mammalian cells and targeted to different subcellular locations, including the nucleus, cytoplasm, and endoplasmic reticulum (ER). High levels of all ER targeted scFv proteins, but not nuclear or cytoplasmic targeted proteins, were found in transfected COS-1 cells. In an attempt to stabilize the proteins, sequences encoding the mouse immunoglobulin CK constant domain were added to each scFv construct. This led to a moderate increase in the cytoplasmic expression of scFv-FRP5.

PMID: 9016757, UI: 97168950

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Other Formats: Links: ☐ Order this document*Oncogene* 1998 Nov 12;17(19):2445-56

Characterization of a new intrabody directed against the N-terminal region of human p53.

Cohen PA, Mani JC, Lane DP

Department of Biochemistry, Medical Sciences Institute, University of Dundee, UK.

Genes encoding the rearranged immunoglobulin heavy and light chain variable regions of DO-1, a monoclonal antibody directed against human p53, have been used to construct a single-chain antibody. DO-1 recognizes an N-terminal epitope in the region involved in the transactivation function of p53 and the binding of Mdm2. The DO-1 single chain scFv expressed in the periplasm of *E. coli* or at the surface of the filamentous phage M13 retained the immunological specificity and affinity of the full length antibody. Furthermore, the DO-1 recombinant antibody was able to inhibit the *in vitro* binding of Hdm2, and was shown to be a powerful protecting agent of p53's DNA binding activity at 37 degrees C. The DO-1 single-chain antibody has been used to construct single-chain intracellular antibodies (intrabodies) for expression in the cytoplasm and the nucleus of mammalian cells. These anti-p53 intrabodies were additionally modified by addition of a Ckappa domain to increase cytoplasmic and nuclear stability. Here we show that expression of the DO-1 single-chain antibody in the H1299 cell line results in an inhibition of p53's transactivation function. The DO-1 intrabody is a useful tool to study those functions of p53 driven by the N-terminal region of the protein.

PMID: 9824155, UI: 99039761

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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:23:21 : Search time 28.25 Seconds

(without alignments)
301.390 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1335

Sequence: 1 QVKIQESGAEIVRSQASVNL.....YCKQSYNLPFRGGTKLEIK 249

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
A.Geneseq_36.*
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	100.0	249	19 W62770	Single chain antih
2	1024.5	77.9	288	20 W82743	Fusion protein p53
3	1024.5	77.9	673	20 W82742	Plasmod p53/55.1s
4	961	73.1	243	19 W60769	Single chain antih
5	955	72.6	535	18 W28491	Human p53 protein
6	955	72.6	535	18 W28492	Human p53 protein
7	951	72.3	580	20 W90217	Bispecific tetra
8	942	71.6	556	20 W90218	Bispecific tetra
9	932.5	70.9	457	19 W37738	Nucleotide sequenc
10	930	70.0	248	20 Y17960	Mouse scfv fragmen
11	921	70.0	248	20 Y17960	Mouse scfv fragmen
12	906	68.9	281	20 W82744	Fusion protein p1c

13	906	68.9	666	20 W82745	Fusion protein (80
14	901	68.5	248	20 Y17965	Mouse scfv fragmen
15	883	67.1	270	16 R75719	MFE-23 antibody
16	880	66.9	268	20 W90222	Anti-B7.2 monosp
17	877.5	66.7	282	18 W35564	HindIII-EcoRI lase
18	877.5	66.7	282	18 W09818	VH4715-linker-VL47
19	877	66.7	553	18 W11508	Single chain anti-
20	877	66.7	553	20 W73223	H22-anti-CEA antib
21	868.5	66.0	532	19 W35565	HindIII-EcoRI lase
22	850	64.6	248	19 W58836	Human CD30 binding
23	849.5	64.6	263	20 W90226	Anti-B7.2 monosp
24	846	64.3	248	19 W63830	Transformant CDM/1
25	842.5	64.1	241	20 Y11882	Amino acid sequenc
26	831.5	63.2	277	14 R39336	scfv fragment enco
27	830	63.1	269	16 R76682	Human ONS-M21 anti
28	830	63.1	269	17 W04387	Chimaeric human/mu
29	828	63.0	238	20 Y21880	Amino acid sequenc
30	823.5	62.6	244	16 R79867	Anti-BGFR single c
31	818	62.2	301	18 W11507	Single chain, huma
32	818	62.2	301	20 W73217	Multispecific sing
33	816.5	62.1	242	16 R79872	Anti-BGFR single c
34	814.5	61.9	244	16 R79873	Anti-BGFR single c
35	814	61.9	273	20 W90224	Anti-B7.1/anti-B7.
36	813.5	61.9	242	16 R79870	Anti-BGFR single c
37	811.5	61.7	246	16 R79869	Anti-BGFR single c
38	809.5	61.6	249	9 P80154	Biosynthetic antib
39	808.5	61.5	244	16 R79868	Anti-BGFR single c
40	807.5	61.4	482	20 Y06915	Amino acid sequenc
41	805	61.2	242	20 Y17961	Mouse scfv fragmen
42	803.5	61.1	483	20 W88099	A protein compri
43	803.5	61.1	483	21 Y57254	Divalent CC49/212
44	803.5	61.1	483	21 Y80924	Bivalent single ch
45	803.5	61.1	486	14 R37649	Sequence of divale

ALIGNMENTS

RESULT 1
W60770
ID W60770 standard; Protein: 249 AA.
XX
AC W60770;
XX
DT 08-SEP-1998 (first entry)
XX
DE Single chain antibody (scfv) D3M that binds to mutant p53 proteins.
XX
XX Single chain antibody; scfv D3M; mouse; p53 protein; oligomerisation;
KW regulatory domain; p53 mutant; H273; W248; G281;
KW p53-dependent trans-activating activity; restoration;
KW tumour-suppressing activity; tumour cell; treatment;
KW hyper-proliferation; cancer; re-stenosis; ss.
XX
OS Mus sp.
XX
PN W09818825-A1.
XX
PD 07-MAY-1998.
XX
PF 27-OCT-1997; 97WO-FR01921.
XX
PR 29-OCT-1996; 96FR-0013176.
XX
PA (RHON) RHONE-POULENC RORER SA.
XX
PI Debussche L, Bracco L;
XX
DR WPI, 1998-272140/24.
XX
DR N-PSDB; V36237.
XX
PT Restoring p53-dependent trans-activating activity to cell containing
mutant p53 - by delivering single-chain antibody specific for the

PT mutant, particularly for treatment of tumours
 XX
 PS Claim 5; Page 32; 54pp; French.
 XX
 CC The present sequence represents a single chain antibody (ScFv) designated
 CC D3M. The antibody binds to an epitope present in the C-terminal region
 CC of the p53 protein that includes oligomerisation and regulatory domains,
 CC specifically between positions 320 and 393. ScFv D3M is directed against
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
 CC introduced into cells containing a mutant p53 protein, p53-dependent
 CC transactivating activity is restored. ScFv D3M is specific for
 CC p53-mutants that have lost tumour-suppressing activity and are present in
 CC tumour cells. It is particularly used to treat hyper-proliferation
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant
 CC and to purify or detect p53.
 XX
 SQ Sequence 249 AA;
 Query Match 100.0%; Score 1315; DB 19; Length 249;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-88;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLQESGAEIVRSASVNSCTASGFENIKDYMHVWKQREEGLEWIGYIDPESGETEY 60
 DB 1 QVQLQESGAEIVRSASVNSCTASGFENIKDYMHVWKQREEGLEWIGYIDPESGETEY 60
 QY 61 APNPGKATYADTSNTAVLHLSTSEDTTYVCNAVITYEYDGYALDYWGQGTIVTV 120
 DB 61 APNPGKATYADTSNTAVLHLSTSEDTTYVCNAVITYEYDGYALDYWGQGTIVTV 120
 QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMSCSSQSLFNSRTRKNYLAHQ 180
 DB 121 SSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMSCSSQSLFNSRTRKNYLAHQ 180
 QY 181 QKPGQSPKVIYMASTRRESGVDPDRFTGSGSGDTFTLTSSVQAEADLAIVYCKQSYLPF 240
 DB 181 QKPGQSPKVIYMASTRRESGVDPDRFTGSGSGDTFTLTSSVQAEADLAIVYCKQSYLPF 240
 QY 241 GGGTKLEIK 249
 DB 241 GGGTKLEIK 249
 RESULT 2
 W82743
 ID W82743 standard; Protein; 288 AA.
 XX
 AC W82743;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Fusion protein pNc4/55.lscfv/CPG2 R6/del EcorI.
 XX
 KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
 KW product; converting enzyme; cell surface antigen; treatment; cancer;
 KW inflammation; rheumatoid arthritis; antibody; produg therapy system.
 XX
 OS Synthetic.
 XX
 PN WO9851787-A2.
 XX
 PD 19-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-GB01294.
 XX
 PR 10-MAY-1997; 97GB-0009421.
 XX
 PA (GENE) ZENECA LTD.
 XX
 PI Blakey DC, Emery SC;
 XX

DR WPI; 1999-059700/05.
 XX N-PSDB; V72064.
 XX
 PT New gene construct expressing conjugate of targeting agent and
 PT product; converting enzyme - useful for, e.g. targeted production of
 PT cytotoxic drug in vivo, especially for treatment of cancer
 XX
 PS Example 15; Page 82; 100pp; English.
 XX
 CC This sequence is a used in a method for obtaining a novel gene construct
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a
 CC cell-targeting group (I) and a heterologous produg-converting enzyme
 CC (II), and (B) is directed to leave the cell for selective localisation
 CC at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a
 CC target site, then administration of (II) is used for targeted release of
 CC cytotoxic drug, specifically for treating cancer but also inflammation
 CC such as rheumatoid arthritis. In situ generation of the targeting
 CC antibody increases selectivity, reducing side effects at normal tissue.
 CC The method is applicable to any antibody-directed enzyme produg therapy
 CC system.
 XX
 SQ Sequence 288 AA;
 Query Match 77.9%; Score 1024.5; DB 20; Length 288;
 Best Local Similarity 77.9%; Pred. No. 3, 4e-67;
 Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;
 QY 1 QVQLQESGAEIVRSASVNSCTASGFENIKDYMHVWKQREEGLEWIGYIDPESGETEY 60
 DB 23 QVQLQESGAEIVRSASVNSCTASGFENIKDYMHVWKQREEGLEWIGYIDPESGETEY 82
 QY 61 APNPGKATYADTSNTAVLHLSTSEDTTYVCNAVITYEYDGYALDYWGQGTIVTV 120
 DB 61 APNPGKATYADTSNTAVLHLSTSEDTTYVCNAVITYEYDGYALDYWGQGTIVTV 120
 QY 83 NEFKKATLVKSSLTETQMDLSLTSSEDSAVYCARETAYGYDD-ANDYWGQGTIVTV 141
 DB 83 NEFKKATLVKSSLTETQMDLSLTSSEDSAVYCARETAYGYDD-ANDYWGQGTIVTV 141
 QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMSCSSQSLFNSRTRKNYLAHQ 180
 DB 142 SSGGGSGGGSGGGSDIELTQSPSSLAWSAGEKVMSCSSQSLFNSRTRKNYLAHQ 201
 QY 181 QKPGQSPKVIYMASTRRESGVDPDRFTGSGSGDTFTLTSSVQAEADLAIVYCKQSYLPF 240
 DB 202 QKPGQSPKVIYMASTRRESGVDPDRFTGSGSGDTFTLTSSVQAEADLAIVYCKQSYLPF 261
 QY 241 GGGTKLEIK 249
 DB 262 GGGTKLEIK 270
 RESULT 3
 W82742
 ID W82742 standard; Protein; 673 AA.
 XX
 AC W82742;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Plasmid pNc4/55.lscfv/CPG2 R6 protein.
 XX
 KW Conjugate; cell targeting; cytotoxic drug; produg-converting enzyme;
 KW cell surface antigen; treatment; cancer; inflammation; antibody;
 KW rheumatoid arthritis; produg therapy system.
 XX
 OS Synthetic.
 XX
 PN WO9851787-A2.
 XX
 PD 19-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-GB01294.
 XX
 PR 10-MAY-1997; 97GB-0009421.
 XX

PA (ZENE) ZENECA LTD.
XX
PI Blakey DC, Emery SC;
XX
DR WPI; 1999-059700/05.
XX
DR N-PSDB; V72059.
XX
PT New gene construct expressing conjugate of targeting agent and
XX
PT produg-converting enzyme - useful for, e.g. targeted production of
XX
PT cytotoxic drug in vivo, especially for treatment of cancer
XX
PS Example 14; Page 78-79; 100pp; English.
XX
CC This sequence is used in a method for obtaining a novel gene construct
XX
CC (A) which expresses, in cells of a mammal, a conjugate (B) of a
XX
CC cell-targeting group (I) and a heterologous produg-converting enzyme
XX
CC (II), and (B) is directed to leave the cell for selective localisation at
XX
CC a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a
XX
CC target site, then administration of (II) is used for targeted release of
XX
CC cytotoxic drug, specifically for treating cancer but also inflammation
XX
CC such as rheumatoid arthritis. In situ generation of the targeting
XX
CC antibody increases selectivity, reducing side effects at normal tissue.
XX
CC The method is applicable to any antibody-directed enzyme produg therapy
XX
CC system.
XX
SQ Sequence 673 AA;

Query Match 77.9%; Score 1024.5; DB 20; Length 673;
Best Local Similarity 77.9%; Pred. No. 8.5e-67;
Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

OY 1 OVKLQSGAEIVRSGASVNLCTASGFNIDYIMHWKORPEGLEWIGYIDPESGETEY 60
DB 20 qvqlqpggaeivrpqgavqgscaksgyftgyvlhwvkqrpqgglewlgvmpstgrdsy 79
OY 61 APNFGKATVTADTSSNTALHLSLSEDTYYCNAVIYREYDGYALDYWGOGTIVY 120
DB 80 nefkfnkatltvksstetajmqsltsedsavycarerayydd-andywgqgtltv 138
OY 121 SSGGGSGGGSGGGSDIELTQSPSSLAIVSAGEKVMSCSSQSLFNSTRKNYLAWQ 180
DB 139 ssgsgsgsgsgsgsgsdieqlsqspslavsaqekvmcskssqslfnstrknylawyq 198
OY 181 QKRGQSPKVIIVASTRESGVDPDRFTGSGGDTFTLTSSVOAEDLAIVYCKOSYNLPTF 240
DB 199 qrpqgspkrllywastrtsgvprftfgsgsgtdftltssvgaedlaivycqsgyltrlf 258
OY 241 GGCTKLEIK 249
DB 259 ggggtkleik 267

RESULT 4
W60769 standard; Protein: 243 AA.
XX
AC W60769;
XX
DT 08-SEP-1998 (first entry)
XX
DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.
XX
KW Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;
XX
KW regulatory domain; p53 mutant; H273; W248; G281;
XX
KW p53-dependent trans-activating activity; restoration;
XX
KW tumour-suppressing activity; tumour cell; treatment;
XX
KW hyper-proliferation; cancer; re-stenosis; ss.
XX
OS Mus sp.
XX
XX WO9818825-A1.
XX

PD 07-MAY-1998.
XX
XX 27-OCT-1997; 97WO-ER01921.
XX
XX 29-OCT-1996; 96FR-0013176.
XX
XX (RHON) RHONE-POULENC RORER SA.
XX
XX Debussche L, Bracco L;
XX
XX WPI; 1998-272140/24.
XX
XX DR N-PSDB; V36236.
XX
PT Restoring p53-dependent trans-activating antibody to cell containing
XX
PT mutant p53 - by delivering single-chain antibody specific for the
XX
XX mutant, particularly for treatment of tumours
XX
PS Claim 5; Page 31; 54pp; French.
XX
CC The present sequence represents a single chain antibody (ScFv) designated
XX
CC 421. The antibody binds to an epitope present in the C-terminal region
XX
CC of the p53 protein that includes oligomerisation and regulatory domains,
XX
CC specifically between positions 320 and 393. ScFv 421 is directed against
XX
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
XX
CC introduced into cells containing a mutant p53 protein, p53-dependent
XX
CC trans-activating activity is restored. ScFv 421 is specific for
XX
CC p53-mutants that have lost tumour-suppressing activity and are present in
XX
CC tumour cells. It is particularly used to treat hyper-proliferation
XX
CC associated with these mutants (e.g. cancer and re-stenosis) but may also
XX
CC be used in vitro for studying mechanisms of activity of p53 or its mutant
XX
CC and to purify or detect p53.
XX
SQ Sequence 243 AA;

Query Match 73.1%; Score 961; DB 19; Length 243;
Best Local Similarity 74.8%; Pred. No. 1.1e-62;
Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;

OY 1 OVKLQSGAEIVRSGASVNLCTASGFNIDYIMHWKORPEGLEWIGYIDPESGETEY 60
DB 1 qvqlqsggaeivrsqasvxlscasgfinkdyhmhwkqrpqgglewlgwidpengtley 60
OY 61 APNFGKATVTADTSSNTALHLSLSEDTYYCNAVIYREYDGYALDYWGOGTIVY 120
DB 61 aprtqgkatmtadtsntalytqsltsasedtavyen-----fydaadygqgtltv 114
OY 121 SSGGGSGGGSGGGSDIELTQSPSSLAIVSAGEKVMSCSSQSLFNSTRKNYLAWQ 180
DB 115 ssgsgsgsgsgsgsgsdvltmqtpdlstvtgqpslsckssqslde-dgktylnwll 173
OY 181 QKRGQSPKVIIVASTRESGVDPDRFTGSGGDTFTLTSSVOAEDLAIVYCKOSYNLPTF 239
DB 174 qrpqgspkrllyvskldsgvprftfgsgsgtdftltklnrveadlgyvycwqgthspit 233
OY 240 FGCTKLEIK 249
DB 234 fgggtkleik 243

RESULT 5
W28491 standard; Protein: 535 AA.
XX
AC W28491;
XX
DT 25-NOV-1997 (first entry)
XX
DE Human p53 protein variant S-325 encoded by pBC176.
XX
XX Leucine zipper domain; LZD; oligomerisation domain; mutant; muten;
XX
XX substitution; replacement; transactivation; viral protein VP16; HSV;
XX
XX anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
XX

KW		tumour suppression; apoptosis; single chain antibody variable domain.
XV		
XX	OS	Chimeric - Homo sapiens.
OS		Chimeric - Herpes simplex virus.
OS		Synthetic.
XX		
PN		WO9704092-A1.
XX		
XX		06-FEB-1997.
PD		
PP		17-JUL-1996; 96MO-FR01111.
PX		
PR		19-JUL-1995; 95FR-0008729.
PA		(RHON) RHONE POULENC RORER SA.
XX		
PI		Braeco L, Conseiller E;
DR		WIPI: 1997-132633/12.
N-		N-PSDB: T86221.
PT		New p53 variants e.g. with oligomerisation domain replaced by
PT		leucine zipper - useful for treating hyper-proliferative disorders,
PT		esp. cancer and restenosis
XX		
PS		Claim 36; Pages 88-90; 133pp; French.
CC		
CC		Claimed variants of protein p53 have at least part of the
CC		oligomerisation domain deleted and replaced by a leucine zipper
CC		domain. The mutants preferably also have at least part of the p53
CC		transactivation domain (amino acids 1-74) deleted and replaced by
CC		the transactivating domain (TAD) from herpes simplex virus viral
CC		protein VP16 (amino acids 411-490) or by a protein domain able to
CC		bind selectively to a transactivator, especially a single-chain
CC		antibody variably domain (ScFv). The present sequence is that of
CC		a specifically claimed p53 variant designated S-325 and comprising
CC		a ScFv domain, amino acids 75-325 of human wild-type p53 and a
CC		leucine zipper domain at the C-terminal. The p53 variants are
CC		more active and more stable tumour suppressors and apoptosis-inducing
CC		agents than wild-type p53 and are active where the wild-type protein
CC		is not, i.e. they are not inactivated by dominant negative or oncogenic
CC		mutants, nor by other cellular proteins (because the leucine zipper
CC		domain prevents formation of inactive mixed oligomers).
XX		
SO		Sequence 535 AA:
		Query Match 72.6%; Score 955; DB 18; Length 535;
		Best Local Similarity 74.4%; Pred. No. 7.2e-62;
		Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;
OY	1	OYKLOESGAEIYRSAGASVALSCTASGFNFKIDYYMHVKQRPDEGLEWMITYPESEGETY 60
Dd	3	GVLQLSSAELIYGSASVGLSLCTASGFNFKIDYYMHVKQRPDEGLEWMITYPESEGETY 62
OY	61	AAPFGGKTATVTADTSNNIVYLHLSLTSEDTVNYCNNAVITYEYGVALDYDGNGRTVV 120
Dd	63	AKPKIGKATMCDTSNTAYIGLISLAEDTAUYCN-----FYGDALDYGSGRTVV 116
OY	121	SSGGGSGGGSGGGSDIELTQSFSILAVSAGEKVAMSKKSQSIFNSRIKKNTLAMWY 180
Dd	117	SSGGSYSGGSGGGSGDSVDLMTCPLTLSTLGPGSAISKESQSILDS-dgktylnwll 175
OY	181	OKPQGSPVLYIYWASTREGVPDRFTGSSGSGNDPFLITISVGAEPLAVYYCKSQSNLP-T 239
Dd	176	GRPGSGPKRLIYLVSKLDSPDIRITGSGSGDTFLIKINVAEDLGYVCWGQHSHPLT 235
OY	240	FEGGGRLEIRK 249
Dd	236	fgaqtklek 245
RESULT	6	

```

W28492
ID W28492 standard; Protein; 535 AA.
XX
XX
AC W28492:
XX
DT 25-NOV-1997 (first entry)
XX
DE Human p53 protein variant S-325H.
XX
KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
KW substitution; replacement; transactivation; viral protein VP16; HSV;
KW anti-oncogene; hyperproliferation; cancer; restenosis; SCFV;
KW tumour suppression; apoptosis; single chain antibody variable domain.
XX
XX Chimeric - Homo sapiens.
OS Chimeric - Herpes simplex virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 361
FT /note="Arg residue at position 182 of wild-type
FT p53 has been mutated to His"
XX
XX
XX W09704092-A1.
XX
XX
XX 06-FEB-1997.
XX
XX
XX 17-JUL-1996; 96WO-FR01111.
XX
XX 19-JUL-1995; 95FR-0008729.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Bracco L, Conseiller E;
XX
XX WPI: 1997-132633/12.
XX
XX
XX New p53 variants e.g. with oligomerisation domain replaced by
XX leucine zipper - useful for treating hyper-proliferative disorders,
XX esp. cancer and restenosis
XX
XX
XX Claim 36; Page -; 133pp; French.
XX
XX
XX Claimed variants of protein p53 have at least part of the
XX oligomerisation domain deleted and replaced by a leucine zipper
XX domain. The mutants preferably also have at least part of the p53
XX transactivation domain (amino acids 1-74) deleted and replaced by
XX the transactivating domain (TP) from herpes simplex virus viral
XX protein VP16 (amino acids 411-490) or by a protein domain able to
XX bind selectively to a transactivator, especially a single-chain
XX antibody variable domain (SCFV). The present sequence is that of
XX a specifically claimed p53 variant designated S-325H and comprising
XX a SCFV domain, amino acids 75-325 of human wild-type p53 (but with
XX Arg182 replaced by His) and a leucine zipper domain at the C-terminal.
XX The p53 variants are more active and more stable tumour suppressors
XX and apoptosis-inducing agents than wild-type p53 and are active where
XX the wild-type protein is not, i.e. they are not inactivated by dominant
XX negative or oncogenic mutants, nor by other cellular proteins (because
XX the leucine zipper domain prevents formation of inactive mixed
XX oligomers).
XX
XX (Note: this sequence does not appear in the specification and has
XX been produced by modifying the given sequence of variant V-325).
XX
XX
XX Sequence 535 AA;
XX
XX
XX Query Match 72.6%; Score 955; DB 18; Length 535;
XX Best Local Similarity 74.4%; Pred. No. 7, 2e-62;
XX Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3
XX
XX
XX 1 QVKIQESAGAEIYRGSASVNLSTAGFNKIDYIMHWKQRPBEGLEWIGYIDPESSEFTEY 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 3 gvgdqesaaeeivsgssavklsctaagihlkdyimhwvkrpbgglewlgwidpeneqddy 62

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OY 61 APNFGKATVADTSSNTAYLHLSLTSEDITVYYCNAYIYYEDGALDYGOGTIVY 120
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 apkfgkatmtcdtsntaylqlssascdtavyccn-----fygdaldygggtttvv 116
OY 121 SSGGGSGGGGGGGSDIELTQSPSSLAVSAGEVAMSCSKSSQSLFNSRTRKNYLAWQ 180
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 117 ssqggsgsgsgsgsdvltmctptltsltlgqpsasickssqslldc-dgktylnwll 175
OY 181 QKPGGSPKVLTYWASTREGVDPDRFTGSGSGDTFTLTSSVQAEADLAAYYCKQSYNLP-T 239
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 176 qrpqgspkrllyvskldsgvdpdrftgsgsgdftlknrvaeedlgyvycwqgthspit 235
OY 240 FCGGTLEIK 249
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 236 fgaqtkleik 245

RESULT 7
W90217
ID W90217 standard; Protein: 580 AA.
AC W90217;
XX 10-MAY-1999 (first entry)
DT 10-MAY-1999 (first entry)
DE Bispecific tetraivalent antibody B1TAB7-24-IG10H6.
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;
XX CD86; T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease;
XX allergy; therapy: human; bispecific tetraivalent antibody; B1TAB;
XX B1TAB7-24-IG10H6.
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX Key Location/Qualifiers
FH Peptide 1..24
FT /note= "peab signal peptide"
FT Region 25..138
FT /note= "VH region anti B7.1 Mab"
FT Peptide 139..153
FT /note= "(GAS3) flexible linker"
FT Region 154..262
FT /note= "VL region anti B7.1 Mab"
FT Region 263..273
FT /note= "human IgG3 hinge region"
FT Domain 274..308
FT /note= "helix-turn-helix dimerisation domain"
FT Domain 309..319
FT /note= "human IgG3 hinge domain"
FT Region 320..446
FT /note= "VH region anti B7.2 Mab"
FT Peptide 447..461
FT /note= "(GAS3) flexible linker"
FT Region 462..574
FT /note= "VL region anti B7.2 Mab"
FT Peptide 575..580
FT /note= "His6 tag"
FT Misc-difference 261
FT /note= "encoded by CNG"
FT Misc-difference 322..327
FT /note= "codons for these amino acids are not
    present in the DNA sequence for
    B1TAB7-24-IG1-H6 provided in the
    specification"
XX W09858965-A2.
XX 30-DEC-1998.

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PF 22-JUN-1998; 98WO-EP03791.
XX 20-JUN-1997; 97EP-0870092.
PR (INNO-) INNOGENETICS NV.
XX Bosman A, Buysse M, Lorre K, Sablon E;
PI WPI: 1999-105615/09.
DR N-PSDB; X01651..
DR New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection
PR Example 7.1; Fig 16; 182pp; English.
XX This polypeptide comprises the bispecific tetraivalent antibody
XX B1TAB7-24-IG10H6. The molecule consists of 4 scfvs, i.e. 2
XX anti B7.1 scfvs and 2 anti B7.2 scfvs (tetravalency). One single
XX B1TAB is a homodimer of 2 identical molecules, each containing both
XX an anti B7.1 and anti B7.2 scfv (bispecificity). An anti-B7.1 and
XX and anti-B7.2 scfv are linked using a dimerisation domain (see
XX W90219), which drives the homodimerisation of the molecule. DNA
XX expression of the B1TAB in transformed E. coli cells. The B1TAB
XX cross-links, and/or cross-reacts, with the costimulatory molecules
XX B7.1 and B7.2 that are expressed on the membrane of professional
XX antigen-presenting cells, leading to the inhibition of antigen-
XX specific T cell activation. The invention relates to such
XX B7-binding molecules, methods for their production, and their use
XX for treating or preventing diseases of the immune system, in
XX particular graft rejection, graft versus host disease, allergy and
XX autoimmune diseases (claimed).
XX Sequence 580 AA:
SQ
Query Match 72.3%; Score 951; DB 20; Length 580;
Best Local Similarity 73.5%; Pred. No 1.5e-61;
Matches 183; Conservative 22; Mismatches 44; Indels 0; Gaps 0;
OY 1 OVKLOESGAELVRSAGAVNLSCTASGFNIKDYMMVWRQPEEGLEWIGYIDPESGETEY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 325 qvqlqsgspellekpgasvkiskcasgydfgmmmwvqngskslwlgldipyrgysv 384
OY 61 APNFGKATVADTSSNTAYLHLSLTSEDITVYYCNAYIYYEDGALDYGOGTIVY 120
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 385 npkifgkatltvdkssstlaymqlsitsdsavycarfaygydyymdywgggtttvv 444
OY 121 SSGGGSGGGGGSDIELTQSPSSLAVSAGEVAMSCSKSSQSLFNSRTRKNYLAWQ 180
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 445 ssqggsgsgsgsgsdvltmctptltsltlgqpsasickssqslldc-dgktylnwll 504
OY 181 QKPGGSPKVLTYWASTREGVDPDRFTGSGSGDTFTLTSSVQAEADLAAYYCKQSYNLP-T 240
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 505 qkpqgspkrllyvskldsgvdpdrftgsgsgdftlknrvaeedlgyvycwqgthspit 564
OY 241 GCGTLEIK 249
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 565 ggaqtkleik 573

RESULT 8
W90218
ID W90218 standard; Protein: 556 AA.
AC W90218;
XX 10-MAY-1999 (first entry)
DT 10-MAY-1999 (first entry)
DE Bispecific tetraivalent antibody B1TAB1G10-B7-24H6.
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;

```

KW CD86; T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease;
 KW allergy; therapy; human; bispecific tetraivalent antibody; B17Ab;
 KW B17Ab1G10-B7-24H6.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 OS Chimeric - synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..120 "VH region anti B7.2 MAb"
 FT Peptide /note="VH region anti B7.2 MAB"
 FT Peptide 121..135
 FT /note="(G4S3) flexible linker"
 FT Region 136..248
 FT /note="VL region anti B7.2 MAB"
 FT Region 249..259
 FT /note="human IgG3 hinge region"
 FT Domain 260..285
 FT /note="helix-turn-helix dimerisation domain"
 FT Domain 286..305
 FT /note="human IgG3 hinge domain"
 FT Region 306..426
 FT /note="VH region anti B7.1 MAB"
 FT Peptide 427..441
 FT /note="(G4S3)flexible linker"
 FT Region 442..550
 FT /note="VL region anti B7.1 MAB"
 FT Peptide 551..556
 FT /note="His6 tag"
 FT
 PN W09858965-A2.
 XX
 PD 30-DEC-1998.
 XX
 PE 22-JUN-1998; 98WO-EP03791.
 XX
 PR 20-JUN-1997; 97EP-0870092.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Bosman A, Buyse M, Lorre K, Sablon E;
 DR WPI: 1999-105615/09.
 DR N-PSDB; X01652.
 XX
 PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 PT immune diseases including allograft rejection
 XX
 PS Example 7.1; Fig 18; 182pp; English.
 XX
 CC This polypeptide comprises the bispecific tetraivalent antibody
 CC B17Ab1G10-B7-24H6. The molecule consists of 4 scFvs, i.e. 2
 CC anti B7.1 scFvs and 2 anti B7.2 scFvs (tetravalency). One single
 CC B17Ab is a homodimer of 2 identical molecules, each containing both
 CC an anti B7.1 and anti B7.2 scFv (bispecificity). An anti-B7.1 and
 CC and anti-B7.2 scFv are linked using a dimerisation domain (see
 CC W90219), which drives the homodimerisation of the molecule. DNA
 CC (see X01652) encoding the B17Ab has been constructed to allow
 CC expression of the B17Ab in transformed E. coli cells. The B17Ab
 CC cross-links, and/or cross-reacts, with the costimulatory molecules
 CC B7.1 and B7.2 that are expressed on the membrane of professional
 CC antigen-presenting cells, leading to the inhibition of antigen-
 CC specific T cell activation. The invention relates to such
 CC B7-binding molecules, methods for their production, and their use
 CC for treating or preventing diseases of the immune system, in
 CC particular graft rejection, graft versus host disease, allergy and
 CC autoimmune diseases (claimed).
 CC
 SQ Sequence 556 AA:

Query Match; 71.6%; Score 942; DB 20; Length 556;

Best Local Similarity 73.3%, Pred. No. 6,5e-61;
 Matches 181; Conservative 22; Mismatches 44; Indels 0; Gaps 0;
 QY 3 KLOESGAEIIVHSGASVNSCTASGFINRKYVMHWKORPEEGLEWIGVDPESGETEYAP 62
 Db 1 q1qgsapelekpgasvksckasgysftgmmwvwxgngkswlglidpyggtsynp 60
 QY 63 NFOGKATVTAJPTSSNTAVLHLSLSLSEDTTYYCNAVYYEYDYGALDYMGOGTTVTSS 122
 Db 61 kiegakellvdkssstajmqlesltsedsavyycaarfaygdgyyldmwygqctvss 120
 QY 123 GCGGSGGSGGSGGSDIELTQSPSSLAWSAGEKVMASCSKSSQSLNSRKRYLWYQOK 182
 Db 121 gggsgsgsgsgsgsdieitqspsslawageevmtckssqsvlyssnqknylawyqk 180
 QY 183 PGSPKVLITVMASTRESGVDPDRFTGSGGTDFLTITSSVQAADLVVYCKOSYNLPTFGG 242
 Db 181 pgspklllyvastresgvpdrftgsggtclstlssqaedlavyychqylsswtfg 240
 QY 243 GTRLEIK 249
 Db 241 gtrleik 247
 RESULT 9
 W37738
 ID W37738 standard; Protein: 437 AA.
 XX
 XX W37738;
 AC
 DT 07-JUL-1998 (first entry)
 DE
 XX Nucleotide sequence encoding the Mgr6-clavin immunotoxin.
 KW Recombinant ribosomal inhibitor protein; RIP; clavin; inhibition;
 KW protein synthesis; conjugate; Mgr6-clavin; anticancer; antiviral agent.
 XX
 OS Chimeric - Aspergillus clavatus.
 OS Chimeric - Mus musculus
 XX
 FH Key Location/Qualifiers
 FT Peptide 96..286
 FT /note="Mgr6 from M. musculus"
 FT Peptide 287..437
 FT /note="Clavin from A. clavatus"
 XX
 PN W09749726-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 26-JUN-1997; 97WO-EP03359.
 XX
 PR 27-JUN-1996; 96IT-FI00155.
 XX
 PA (ITUV-) ITAL MIN UNIV RICECA SCI & TECNOLOGICA.
 PI Colnaghi M, De Santis R, Mele A, Parente D;
 DR WPI: 1998-077109/07.
 DR N-PSDB; V09256.
 XX
 PT DNA encoding Aspergillus clavatus-derived ribosomal inhibitor
 PT protein, clavin - useful as an immuno-conjugate and for treatment of
 PT cancer
 XX
 PS Claim 4; Pages 14-15; 26pp; English.
 XX
 CC This is the amino acid sequence of a fusion protein comprising of the
 CC Mgr6 single chain antibody (with the heavy and light chain joined by
 CC a linker), fused to the clavin protein. Clavin is an inhibitor
 CC protein, and functions by inactivating the ribosomes. Clavin or its
 CC conjugates are useful as anticancer and/or antiviral agents. The
 CC recombinant ribosomal inhibitor protein (RIP), Mgr6-clavin (a conjugate

CC of clavlin) is used as an immunoconjugate, and the complex and clavlin
CC alone are capable of inhibiting ribosomal activity.

SQ Sequence 437 AA;

Query Match	70.9%	Score 932.5	DB 19	Length 437
Best Local Similarity	72.8%	Pred NO.2.4e-60		
Matches 182	Conservative 25	Mismatches 36	Indels 7	Gaps 4

OY	1	QVKLOESAEVLVRSGASVNLCTASGFINKDYVMHWKQREBELEWIGYIDPESETEX	60
Db	37	qvqfqesgaetlvkpgasvxlscstasgfinkctlymhvkqrppegglwrlgrldpanqrthy	96
OY	61	APNFOGKATVTADTSSNTAYLHLSSLSEDTFTVYYCNAVIYYERYDGLADWDGGCTTVY	120
Db	97	dprfsgktcltadcsnraylqlslstedcavyycc--argeyd-yfpfwgqgststv	153
OY	121	SSGGGSGCGSGGGGSDIELTOSPSLSAVAGSKVMSCKSQSOLNSRFRKKYALMYQ	180
Db	153	ssggsgsgsgsgsgsgsgyietltgpaaavaqlgratlstcaasgv--stearysmymvq	210
OY	181	QKPQSGPKVLLYWASTRESGYPDHRTGSAGSCTDFLTLISSVOAEDLAVYCKCKOGYNP-T	233
Db	211	qkpqpdpklltkysanlesgyparfsgsgsfdfllnhpwecedeatycqhsewelprr	270
OY	240	EGGSGKTLEIK 249	
Db	271	tfgggtklleik 280	

RESULT	10
Y17960	
ID	Y17960 standard; Protein; 248 AA.

AC Y17960;

DT 04-AUG-1999 (first entry)

DE Mouse scFV fragment 4-1.

KM Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer
KM autoimmune disease; scFv-antibody; single-chain Fv; mouse.

Mus sp.

PN WO9925818-A1.

PD 27-MAY-1999

PF 16-NOV-1998; 98WO-EP07313

PR 17-NOV-1997; 97EP-0120096

PA (KUFE/) KUFER P.

PI Borschert K, Kufer P, Lutterbuese R, Raum T, Zettl F;

DR WPI: 1999-338004/28.

XX

PT retaining capacity to bind an epitope

PS Claim 27; Fig 6.6; 152pp; English.

CC The invention relates to a method

CC The invention relates to a method of identifying binding site domains:
CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi
CC multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD

CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides on
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method. Sequences Y17957-965 represent
CC mouse scFv fragments.

SQ Sequence 248 AA;

Query Match	70.7%	Score 930;	DB 20;	Length 248;
Best Local Similarity	72.9%	Pred. No. 2e-60;		
Matches 180;	Conservative 25;	Mismatches 38;	Indels 4;	Gaps 2

OY	4	LOESSALVETRSGASVNISCTASGNINRDMXYHMHWKOREBELEWIGYIDPSSGTEVAFN	63
Dd	5	IegsaeealvrgtstsktsckasgyafcnuygwwkqipngliewgdafipssgnahyneK	64
OY	64	FQGRATVADTSSNTAYLHLHSLSLTSEDTYYVCNAVITYEEDYGALDWDGCGTTVTYSG	122
Dd	65	fkgaelrladksrsytaymqsltsesedavyfcarlnmwd--eamdwygggtlvvtvsq	123
OY	124	GGSGGGGGSGGGSDIELTOSPSSLASAGCKVAMSCCKSSSLNSNRKKUYIWMYOOKP	180
Dd	122	ggsgsgsgsgsgsgselwmtcgspsslsvaaagelvmnscskssgllnsqdknylwmyqkp	181
OY	184	GOSPKVLTYMARSREBSGVDPDRFTTGSGGTDETLTISSVOAEDLAVVYCOKOSYNLP-TEGC	242
Dd	182	ggppkllylgssstresgvpdrtftgsqsgdtcltlissvgaedelavvyqcndhsyplvltfg	243
OY	243	GTKLEIK	249
Dd	242	gtkleik	248

RESULT	11
Y17964	
ID	Y17964 standard; Protein; 248 AA

AC Y17964;

DT. 04-AUG-1999 (first entry)

DE Mouse scFv fragment 5-10

KM Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.

Mus sp.

PN W09925818-A1

PD 27-MAY-19
YY

16-NOV-1998; 38WO-EP07313.

PR : 17-NOV-1997; 37EP-0120096.

PA (KUE/) KUEP P.

.. Borschert K, Küter P, Lutterbuese R, Raum T, Zettl F,
 .pl Borschert K, Küter P, Lutterbuese R, Raum T, Zettl F,
 .xy

DR WPL: 1999-338604/28.
DB N-PSDB: Y77247

Pharmacokinetic

PI Retaining capacity to bind an epitope

PS Claim 27; Fig 6.10; 152pp; English.

XX The invention relates to a method of identifying binding site domains
 CC (BSD) that retain the capacity of binding to a predetermined epitope when
 CC positioned C-terminal of at least one further domain in a recombinant di-
 CC or multivalent polypeptide. The method comprises (a) testing a panel of
 CC BSD displayed on the surface of a biological display system as part of a
 CC fusion protein for binding to a predetermined epitope, where the fusion
 CC protein comprises an additional domain positioned N-terminal of the BSD
 CC and an amino acid sequence that mediates anchoring of the fusion protein
 CC to the surface of the display system; and (b) identifying a BSD that
 CC binds to the predetermined epitope. The method is useful to identify bi-
 CC or multivalent polypeptides that comprise antibody binding sites capable
 CC of efficiently binding to the corresponding antigen. The polypeptides or
 CC antibodies identified by the method are useful therapeutically and
 CC diagnostically, for e.g. cancer and autoimmune diseases. scFv-antibody
 CC fragments that bind independently of their position within bifunctional
 CC single-chain fusion proteins can be isolated from combinatorial antibody
 CC libraries using the new in vitro method. Sequences Y1/957-965 represent
 CC mouse scFv fragments.

SO Sequence 248 AA:

Query Match 70.0%; Score 921; DB 20; Length 248;
 Best Local Similarity 71.7%; Pred. No. 9e-60;
 Matches 177; Conservative 25; Mismatches 41; Indels 4; Gaps 2;

QY 4 LOSGSAELVRSAGSVNLCTASGFNFKDYMHVWKORPEGLEWIGYIDPESGETEAPN 63
 Bb 5 leqsgaelvyrpgrsvskscasgafnlyvkwkpgphglewlgdlfpqsgnlhynek 64
 QY 64 FQKATVTAADTSSNTAVLHLSLTSEDTYYVCNAVYYEYDGYALDYGQGTVTWSSG 123
 Bb 65 fkgkaltldkssstymqslstfedsavfcarlnw---epndywgqgtvtvssg 121
 QY 124 GGGSGGGSGGGSDIELTOSPSLAVSAGEKYAMCKSSQSLFNSRTKKNYLAWQKP 183
 Bb 122 gggsgggsgggsggslvmtqspslvtatagekytmsckssqslinsgqknyltwygqkp 181
 QY 184 GQPKVLIWASTRESGVDPDRFTGSGSGTDFLTLTSSVOAEDLAVYCKOSYMLP-TFGG 242
 Bb 182 gqpkvlliywastresgvdpdrftgsgsgtdfcltltssvgaedlavyycqndysyplftga 241
 QY 243 GTKLEIK 249
 Bb 242 gtlkleik 248

RESULT 12
 W82744
 ID W82744 standard; Protein: 281 AA.
 XX
 AC W82744;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Fusion protein pIC1266/8061scFvtag/his.
 XX
 KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
 KW produg-converting enzyme; cell surface antigen; treatment; cancer;
 KW inflammation; rheumatoid arthritis; antibody; produg therapy system.
 XX
 OS Synthetic.
 XX
 PN WO9851787-A2.
 PD 19-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-GB01294.
 XX
 PR 10-MAY-1997; 97GB-0009421.
 XX

PA (ZENEC) ZENECA LTD.
 XX
 PI Blakey DC, Emery SC;
 XX
 DR WPI: 1999-059700/05.
 XX
 DR N-PSDB; V72069.
 XX
 PT New gene construct expressing conjugate of targeting agent and
 PT produg-converting enzyme - useful for, e.g. targeted production of
 PT cytotoxic drug in vivo, especially for treatment of cancer.
 XX
 PS Example 16; Page 84-85; 100pp; English.

XX This sequence is a used in a method for obtaining a novel gene construct
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a
 CC cell-targeting group (I) and a heterologous produg-converting enzyme
 CC (II), and (B) is directed to leave the cell for selective localisation
 CC at a cell surface antigen (Ag) recognised by (I). Delivery of (B) to a
 CC target site, then administration of (II) is used for targeted release of
 CC cytotoxic drug, specifically for treating cancer but also inflammation
 CC such as rheumatoid arthritis. In situ generation of the targeting
 CC antibody increases selectivity, reducing side effects at normal tissue.
 CC The method is applicable to any antibody-directed enzyme produg therapy
 CC system.

SO Sequence 281 AA:

Query Match 68.9%; Score 906; DB 20; Length 281;
 Best Local Similarity 69.2%; Pred. No. 1.3e-58;
 Matches 173; Conservative 30; Mismatches 37; Indels 10; Gaps 3;

QY 1 OVALLSGSAELVRSAGSVNLCTASGFNFKDYMHVWKORPEGLEWIGYIDPESGETEY 60
 Bb 23 evqlqsggaelvyrsgasvnlctasgfnldknyhmvkkrpgglewlmwldpengdtey 82
 QY 61 APNFOGKATVTAADTSSNTAVLHLSLTSEDTYYVCNAVYYEYDGYALDYGQGTVTW 120
 Bb 83 apftrgkaltldkssstymqslstfedsavfcarlnw---epndywgqgtvtvssg 140
 QY 121 SSGGGSGGGSGGGSDIELTOSPSLAVSAGEKYAMCKSSQSLFNSRTKKNYLAWQKP 180
 Bb 141 ssgggsgggsgggsggslvltqspalmsapgekvtltcsassv-----tymhwtdg 193
 QY 181 QKFGQSPKVLWASTRESGVDPDRFTGSGSGTDFLTLTSSVOAEDLAVYCKOSYMLP-T 239
 Bb 194 qkfgtspkvlwystnlasgvpdrftgsgsgtaltltssmaedaatlycqgrsypplt 253
 QY 240 FGGGTLEIK 249
 Bb 254 fgagtkleik 263

RESULT 13
 W82745
 ID W82745 standard; Protein: 666 AA.
 XX
 AC W82745;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Fusion protein (806.077 scFv-CPG2).
 XX
 KW Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
 KW produg-converting enzyme; cell surface antigen; treatment; cancer;
 KW inflammation; rheumatoid arthritis; antibody; produg therapy system.
 XX
 OS Synthetic.
 XX
 PN WO9851787-A2.
 PD 19-NOV-1998.
 XX

[illegible]

27-MAY-1999.
16-NOV-1998; 98WO-EP07313.
17-NOV-1997; 97EP-0120096.
(KUFE/) KUFER P.
Borschert K, Kufer P, Lutterbuese R, Raum T, Zetl F,
WPI: 1999-338004/28.
N-PSDB; X77248.
Phase display system for identification of binding site domains
retaining capacity to bind an epitope
Claim 27; Fig 7; 152pp; English.
The invention relates to a method of identifying binding site domains
(BSD) that retain the capacity of binding to a predetermined epitope when
positioned C-terminal of at least one further domain in a recombinant bi-
or multivalent polypeptide. The method comprises (a) testing a panel of
BSD displayed on the surface of a biological display system as part of a
fusion protein for binding to a predetermined epitope, where the fusion
protein comprises an additional domain positioned N-terminal of the BSD
and an amino acid sequence that mediates anchoring of the fusion protein
to the surface of the display system; and (b) identifying a BSD that
binds to the predetermined epitope. The method is useful to identify bi-
or multivalent polypeptides that comprise antibody binding sites capable
of efficiently binding to the corresponding antigen. The polypeptides or
antibodies identified by the method are useful therapeutically and
diagnostically, for e.g. cancer and autoimmune diseases. Scfv-antibody
fragments that bind independently of their position within bifunctional
single-chain fusion proteins can be isolated from combinatorial antibody
libraries using the new in vitro method. Sequences Y1957-965 represent
mouse scfv fragments.

```

Query Match Similarity      68.5%; Score 901; DB 20; Length 248;
Best Local Similarity      70.9%; Pred. No. 2,5e-58;
Matches 175; Conservative 27; Mismatches 41; Indels 4; Gaps 2

QY      4  LQESGAELVRSASVSNLCTASGENIKDYIMHWKORPEEGLEWICIDPESGETEYAPN 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      5  LQESGAELVRSASVSNLCTASGENIKDYIMHWKORPEEGLEWICIDPESGETEYAPN 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      64  FQGRATVADTSSNFAVLEHLSLTSEDTFVVCNNAVITYEYOGVALDWDYGQGTTVSSG 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65  FQGRATVADTSSNFAVLEHLSLTSEDTFVVCNNAVITYEYOGVALDWDYGQGTTVSSG 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      124  GGGSGGGSGGSGSDIELTQSPSSLAVSAGEEVAMSCSKSSQSLFNSRTKKNLYAQKP 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      122  GGGSGGGSGGSGSDIELTQSPSSLAVSAGEEVAMSCSKSSQSLFNSRTKKNLYAQKP 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      184  GQSPKYLIVMASTRGSGVDPRFTGSGSGDTFLTITSSVQAEPLAVYYCKQSYNLP-TFEG 242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      182  GQSPKYLIVMASTRGSGVDPRFTGSGSGDTFLTITSSVQAEPLAVYYCKQSYNLP-TFEG 241
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      243  GTKLEIK 249
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      242  GTKLEIK 248
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ID      R75719
R75719 standard; Protein; 270 AA.
AC      R75719;
XX
XX
DT      26-JAN-1996 (first entry)

```

XX MFE-23 antibody.
 DE encoding CDNA) were selected. This sequence was found to have good
 XX specificity and affinity for CEA, meaning that it can be used in targeted
 CC anti-tumour therapies. A humanised antibody with the complementarity
 CC determining regions of MFE-23 may be produced by CDR grafting. The
 CC antibody may be used for the treatment by surgery or therapy of a
 CC colorectal tumour, or in the diagnosis of a colorectal tumour. MFE-23
 CC may also be used to make diabodies (bivalent or bispecific antibody
 CC fragments which bind to two different antigens), and may be linked to an
 CC antitumour agent or a detectable label.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 27..267
 FT Region /note="variable region"
 FT Region 27..146
 FT Region /note="variable heavy chain"
 FT Region 162..267
 FT Region /note="variable light chain"
 FT Region 27..51
 FT Region /note="FR H1"
 FT Region 52..61
 FT Region /note="CDR H1"
 FT Region 62..75
 FT Region /note="FR H2"
 FT Region 76..85
 FT Region /note="CDR H2"
 FT Region 86..124
 FT Region /note="FR H3"
 FT Region 125..135
 FT Region /note="CDR H3"
 FT Region 136..146
 FT Region /note="FR H4"
 FT Region 147..161
 FT Region /note="linker"
 FT Region 162..184
 FT Region /note="FR L1"
 FT Region 185..194
 FT Region /note="CDR L1"
 FT Region 195..209
 FT Region /note="FR L2"
 FT Region 210..216
 FT Region /note="CDR L2"
 FT Region 217..248
 FT Region /note="FR L3"
 FT Region 249..257
 FT Region /note="CDR L3"
 FT Region 258..267
 FT Region /note="FR L4"
 XX
 PN W09515341-A1.
 PD 08-JUN-1995.
 XX
 PF 05-DEC-1994; 94WO-GB02658.
 XX
 PR 03-DEC-1993; 93GB-0024807.
 XX
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI Begent RHJ, Chester KA, Hawkins RE;
 XX
 DR WPI: 1995-215234/28.
 N-PSDB; Q90663.
 XX
 PT Antibody for carcinoembryonic antigen - for treatment and diagnosis
 PT of colorectal cancer
 XX
 PS Claim 3: Page 48-49; 72pp; English.
 XX
 CC This sequence represents the MFE-23 antibody, which is an antibody
 CC against carcinoembryonic antigen (CEA). CEA is a marker antigen for
 CC cancer imaging and therapy. The MFE-23 antibody sequence was obtained
 CC using phage technology. In this process, mice were immunised with CEA.
 CC The antibody variable region genes obtained from these mice were then
 CC amplified from cDNA and cloned as a single chain Fv (scFv) into
 CC bacteriophage vectors, producing a library. The phages that bound to

CC biotinylated CEA were selected and amplified, and this sequence (and the
 CC encoding CDNA) were selected. This sequence was found to have good
 CC specificity and affinity for CEA, meaning that it can be used in targeted
 CC anti-tumour therapies. A humanised antibody with the complementarity
 CC determining regions of MFE-23 may be produced by CDR grafting. The
 CC antibody may be used for the treatment by surgery or therapy of a
 CC colorectal tumour, or in the diagnosis of a colorectal tumour. MFE-23
 CC may also be used to make diabodies (bivalent or bispecific antibody
 CC fragments which bind to two different antigens), and may be linked to an
 CC antitumour agent or a detectable label.
 XX
 SQ Sequence 270 AA;
 Query Match 67.1%; Score 883; DB 16; Length 270;
 Best local Similarity 67.1%; Pred. No. 5,6e-57;
 Matches 171; Conservative 28; Mismatches 36; Indels 20; Gaps 4;
 QY 1 QVKLQSSGAEIYRSGASVNLCTASGFNIKDYMHVKKRPEGLWIGIDPESGETEY 60
 DB |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
 27 qvllqsggaeivrsgrsvklsctasgfnlksymhlrgsppegglawlgldpengdley 86
 QY 61 APYFOGKATVEADTSNTAYLHLSITSEDTYYVCNAVYYEYDG-----YALDYWGOG 115
 DB |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
 87 apfkgkafitdtsntaylqlssltseclavyyen-----egtpcpyyfdywgqg 139
 QY 116 TWTVSSGGGSGGSGGSGGSDIELTQSPSSLAVSAGEKVMASCKSSQSLFNSRTRKNY 175
 DB |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
 140 ttvtvssggsgsgsgsgsgsenvtlqspalmsaspgkvtlscassv-----sy 192
 QY 176 LAMVQKPGQSPKVLIVMASTRESGVDPDRFTGSGSTDTLTITSSVQADLAVYIKQST 235
 DB :|||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
 193 mhvfqgkpgtspklwlystsnlasgyparfsgsgstysltismeeadaatyqcgrs 252
 QY 236 NLP-TRFGGTKEIK 249
 DB :|||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
 253 syplltgagtklelk 267

Search completed: February 12, 2001, 15:23:23
 Job time: 38 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:26:21 ; Search time 76.8 seconds

(Without alignments)
489.138 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315

Sequence: 1 OVKLOESGAEIVRSGASVNL.....YCKOSYNLPTFGGKLEIK 249

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 924906 seqs, 150866555 residues

Total number of hits satisfying chosen parameters: 924906

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/paa/US06.COMB.pep:*
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22: /cgn2_6/ptodata/2/paa/US097.COMB.pep:*
23: /cgn2_6/ptodata/2/paa/US097.COMB.pep:*
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26: /cgn2_6/ptodata/2/paa/US097.COMB.pep:*
27: /cgn2_6/ptodata/2/paa/US097.COMB.pep:*
28: /cgn2_6/ptodata/2/paa/US097.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315	100.0	249	US-09-297-181-4	Sequence 4, Appli
2	961	73.1	243	US-09-297-181-2	Sequence 2, Appli
3	955	72.6	535	US-08-983-035-38	Sequence 38, Appli
4	951	72.3	580	US-09-468-029-58	Sequence 58, Appli
5	942	71.6	556	US-09-468-029-60	Sequence 60, Appli

6	923.5	70.2	242	19	US-09-594-985A-5	Sequence 5, Appli
7	917.5	69.8	238	19	US-09-559-019-28	Sequence 28, Appli
8	913.5	69.5	240	19	US-09-559-019-27	Sequence 27, Appli
9	906	68.9	262	19	US-09-594-985A-4	Sequence 4, Appli
10	897	68.2	271	19	US-09-594-985A-6	Sequence 6, Appli
11	896.5	68.2	272	19	US-09-594-985A-7	Sequence 7, Appli
12	880	66.9	268	18	US-09-468-029-68	Sequence 68, Appli
13	877	66.7	553	17	US-09-364-088-16	Sequence 16, Appli
14	877	66.7	553	19	US-09-523-279-16	Sequence 16, Appli
15	877	66.7	553	27	US-09-188-082-16	Sequence 16, Appli
16	849.5	64.6	263	18	US-09-468-029-76	Sequence 76, Appli
17	846	64.3	248	13	US-08-996-140-23	Sequence 23, Appli
18	842.5	64.1	241	16	US-09-202-000-8	Sequence 8, Appli
19	830	63.1	269	10	US-08-646-265A-109	Sequence 109, App
20	830	63.1	269	10	US-08-646-265A-109	Sequence 109, App
21	828	63.0	238	16	US-09-202-000-2	Sequence 2, Appli
22	824.5	62.7	245	27	US-09-523-095A-40	Sequence 40, Appli
23	824.5	62.7	271	27	US-09-523-095A-34	Sequence 34, Appli
24	824.5	62.7	274	27	US-09-523-095A-32	Sequence 32, Appli
25	824	62.7	251	1	PCT-US00-19843-11	Sequence 11, Appli
26	824	62.7	251	1	PCT-US00-19843-15	Sequence 15, Appli
27	824	62.7	264	1	PCT-US00-19843-8	Sequence 8, Appli
28	823.5	62.6	244	9	US-08-553-497-20	Sequence 20, Appli
29	822.5	62.5	271	27	US-09-523-095A-30	Sequence 30, Appli
30	822.5	62.5	274	27	US-09-523-095A-26	Sequence 26, Appli
31	822	62.5	301	19	US-09-523-279-14	Sequence 14, Appli
32	818	62.2	301	17	US-09-364-088-14	Sequence 14, Appli
33	818	62.2	301	27	US-09-188-082-14	Sequence 14, Appli
34	816.5	62.1	242	9	US-08-553-497-30	Sequence 30, Appli
35	814.5	61.9	244	9	US-08-553-497-32	Sequence 32, Appli
36	814	61.9	273	18	US-09-468-029-72	Sequence 72, Appli
37	813.5	61.9	242	9	US-08-553-497-26	Sequence 26, Appli
38	811.5	61.5	246	9	US-08-553-497-24	Sequence 24, Appli
39	808.5	61.5	244	9	US-08-553-497-22	Sequence 22, Appli
40	803.5	61.1	259	18	US-09-419-788-115	Sequence 115, App
41	803.5	61.1	483	3	US-07-989-846B-19	Sequence 19, Appli
42	803.5	61.1	483	7	US-08-392-338-19	Sequence 19, Appli
43	803.5	61.1	483	18	US-09-443-213-19	Sequence 19, Appli
44	800.5	60.3	242	9	US-08-553-497-28	Sequence 28, Appli
45	799.5	60.8	241	14	US-09-000-802-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-09-297-181-4
; Sequence 4, Application US/09297181
; GENERAL INFORMATION:
; APPLICANT: Bracco, Laurent
; APPLICANT: Debussche, Laurent
; TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES
; FILE REFERENCE: ST96030-US
; CURRENT APPLICATION NUMBER: US/09/297,181
; CURRENT FILING DATE: 1999-04-26
; EARLIER APPLICATION NUMBER: PCT/FR97/01921
; EARLIER FILING DATE: 1997-10-27
; EARLIER APPLICATION NUMBER: FR96/13176
; NUMBER OF SEQ. ID NOS: 4
; SOFTWARE: Patentia Ver. 2.0
; SEQ ID NO 4
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mgs musculus
US-09-297-181-4

Query Match 100.0%; Score 1315; DB 16; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.2e+08;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 OVKLOESGAEIVRSGASVNLSTASGFNIKDYMHVWKPPEGLWIGYIDPESGETEV 60

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DB 1 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 60
    1 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 60
DB 61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
    61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
DB 61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
    61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
DB 121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
    121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
DB 121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
    121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
DB 181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
    181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
DB 181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
    181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
DB 241 GGGTKLEIK 249
    241 GGGTKLEIK 249
DB 241 GGGTKLEIK 249
    241 GGGTKLEIK 249

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RESULT 2

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US-09-297-181-2
; Sequence 2, Application US/09297181
; GENERAL INFORMATION:
; APPLICANT: Bracco, Laurent
; APPLICANT: Debussche, Laurent
; TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES
; FILE REFERENCE: ST96030-US
; CURRENT APPLICATION NUMBER: US/09/297, 181
; CURRENT FILING DATE: 1999-04-26
; EARLIER APPLICATION NUMBER: PCT/FR97/01921
; EARLIER FILING DATE: 1997-10-27
; EARLIER APPLICATION NUMBER: FR96/13176
; EARLIER FILING DATE: 1996-10-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-297-181-2

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Query Match 73.1%; Score 961; DB 16; Length 243;
Best Local Similarity 74.8%; Pred. No. 3e-77;
Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;

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    1 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 60
DB 1 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 60
    1 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 60
DB 61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
    61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
DB 61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
    61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
DB 121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
    121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
DB 121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
    121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
DB 181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
    181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
DB 181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
    181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
DB 241 GGGTKLEIK 249
    241 GGGTKLEIK 249
DB 241 GGGTKLEIK 249
    241 GGGTKLEIK 249

```

RESULT 3

```

US-08-983-035-38
; Sequence 38, Application US/08983035
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, Emmanuel

```

```

; APPLICANT: BRACCO, Laurent
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcole Road, Mailstop 3C43
; CITY: Collegetville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983, 035
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/08729
; FILING DATE: 19-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR96/01111
; FILING DATE: 17-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky Esq., Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST95044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3816
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-983-035-38

```

```

Query Match 72.6%; Score 955; DB 13; Length 535;
Best Local Similarity 74.4%; Pred. No. 2.7e-76;
Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;

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```

DB 1 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 60
    1 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 60
DB 3 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 62
    3 0VKLOESGAEIVRSAGASVNLSTCTASGFNIKDYMHVWKORPEEGLEWIGYIDPESGETEV 62
DB 61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
    61 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 120
DB 63 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 116
    63 APNFGKATVYADTSSMTAYLHLSTLSEDTTYVCNAVITYEYDGYALDWMGGCTVTV 116
DB 121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
    121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
DB 121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
    121 SSGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMSCSKSSQSLFNSRTKKNYLA MYQ 180
DB 181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
    181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
DB 181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
    181 OKPGOSPKVLIYMASTRESGVDPDRFTGSGGTDFTLTISSVOAEDLAVYCKOSYNLPTE 240
DB 241 GGGTKLEIK 249
    241 GGGTKLEIK 249
DB 241 GGGTKLEIK 249
    241 GGGTKLEIK 249

```

RESULT 4

```

US-09-468-029-58
; Sequence 58, Application US/09468029
; GENERAL INFORMATION:
; TITLE OF INVENTION: B7-Binding molecules for treating immune

```

```

; TITLE OF INVENTION: diseases.
; NUMBER OF SEQUENCES: 80
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/468,029
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP98/03791
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-468-029-58

```

```

Query Match          72.3%; Score 951; DB 18; Length 580;
Best Local Similarity 73.5%; Pred. No. 6.8e-76;
Matches 183; Conservative 22; Mismatches 44; Indels 0; Gaps 0;

```

```

QY 1 QVLOESGAEIVRSASVNLCTASGFNIDYMHVWKQREPEGLWIGYIDPESGETEY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 325 QVLOQSGPELEKPGASVYKISCKASGYFTGHNMNWKQSGKSLWIGIIDPYGGTSY 384
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 APNFGKATVTAATSSNTATLHLSLTSEDTTYVCNAVITYEEDGALDYWGQGTIVY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 385 NPFEGKATITLVKSSSTAYMOLESLTSEDSAVYTCARFAYYDYYIMDYWGQGTIVY 444
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMASCKSSQSLFNSRTKKNYLAWYQ 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 445 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEEYMTCKSSQSLYSSNOKNYLAWYQ 504
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 QKPGSPKVLIIYMASTRRESGVPDRFTSGSGTDEFTLTISVQAEDLAIVYCKOSYLPFG 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 505 QKGGSPKVLIIYMASTRRESGVPDRFTSGSGTDEFTLTISVQAEDLAIVYCHQYLSWTF 564
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 GGGTKLEIK 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 565 GGGTKLEIK 573

```

```

RESULT 5
US-09-468-029-60
; Sequence 60, Application US/09468029
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: B7-Binding molecules for treating immune
; TITLE OF INVENTION: diseases.
; NUMBER OF SEQUENCES: 80
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/468,029
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP98/03791
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 556 amino acids
; TYPE: amino acid

```

```

; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-468-029-60

```

```

Query Match          71.6%; Score 942; DB 18; Length 556;
Best Local Similarity 73.3%; Pred. No. 4.1e-75;
Matches 181; Conservative 22; Mismatches 44; Indels 0; Gaps 0;

```

```

QY 3 KLOESGAEIVRSASVNLCTASGFNIDYMHVWKQREPEGLWIGYIDPESGETEYAP 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 QVLOQSGPELEKPGASVYKISCKASGYFTGHNMNWKQSGKSLWIGIIDPYGGTSY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63 NFGKATVTAADTSSNTATLHLSLTSEDTTYVCNAVITYEEDGALDYWGQGTIVY 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 KFGKATITLVKSSSTAYMOLESLTSEDSAVYTCARFAYYDYYIMDYWGQGTIVY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 123 GGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMASCKSSQSLFNSRTKKNYLAWYQ 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 GGGSGGGSGGGSDIELTQSPSSLAVSAGEEYMTCKSSQSLYSSNOKNYLAWYQ 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 183 PGSPKVLIIYMASTRRESGVPDRFTSGSGTDEFTLTISVQAEDLAIVYCKOSYLPFG 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 PGSPKVLIIYMASTRRESGVPDRFTSGSGTDEFTLTISVQAEDLAIVYCHQYLSWTF 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 243 GTKLEIK 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 241 GTKLEIK 247

```

```

RESULT 6
US-09-594-985A-5
; Sequence 5, Application US/09594985A
; GENERAL INFORMATION:
; APPLICANT: Bardeira-Guillem, Emilio
; TITLE OF INVENTION: Vaccine formulations and methods for immunizing an
; TITLE OF INVENTION: individual against shed antigen-specific B cells
; FILE REFERENCE: 3-25np
; CURRENT APPLICATION NUMBER: US/09/594,985A
; CURRENT FILING DATE: 2000-09-12
; PRIORITY APPLICATION NUMBER: US 60/139,521
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Wordperfect
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: synthesized
US-09-594-985A-5

```

```

Query Match          70.2%; Score 923.5; DB 19; Length 242;
Best Local Similarity 70.0%; Pred. No. 6.2e-74;
Matches 175; Conservative 29; Mismatches 37; Indels 9; Gaps 2;

```

```

QY 1 QVLOESGAEIVRSASVNLCTASGFNIDYMHVWKQREPEGLWIGYIDPESGETEY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 QVLOESGAEIVRSASVNLCTASGFNIDYMHVWKQREPEGLWIGYIDPESGETEY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 APNFGKATVTAATSSNTATLHLSLTSEDTTYVCNAVITYEEDGALDYWGQGTIVY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 NEFKKATITLVKSSSTAYMOLESLTSEDSAVYFCRSTY-----GHWGQGTIVY 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMASCKSSQSLFNSRTKKNYLAWYQ 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```



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Db      253  FGAGTKLVK  262
          || |||| :|

```

RESULT 10
US-09-594-985A-6

```

Sequence 6 Application US/09594985A
GENERAL INFORMATION:
APPLICANT: Barbera-Guillem, Emilio
APPLICANT: Nelson, M. Bud
TITLE OF INVENTION: Vaccine formulations and methods for immunizing an
TITLE OF INVENTION: Individual against shed antigen-specific B cells
FILE REFERENCE: B-2ndp
CURRENT APPLICATION NUMBER: US/09/594,985A
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: US 60/139,521
PRIOR FILING DATE: 1999-06-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: WordPerfect
SEQ ID NO 6
LENGTH: 271
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: synthesized
US-09-594-985A-6

```

Query Match	68.28;	Score 897;	DB 19;	Length 271;
Best Local Similarity	66.98;	Pred. No. 1.6e-71;		
Matches 172;	Conservative 31;	Mismatches 38;	Indels 16;	Gaps 3

```

QY 1 OVKLOESAEELVRSAGASVNLSCSTASGFNFKRYVHWWKOREPELEWIGYIDPSSGETEY 60
D 23 OVULOQSOAEELVRCGASVKISCRKASGTFYDHALHMAKQKREGELEWIGIISPENDIKY 82
QY 61 APNFOGKATVADTADTSSNTAYLHLHSLTSEDITYVCNAVIYEYDYALDIWOGGTVTV 120
D 83 NEKFKRGKATLTADRSSTSYAYMQLNLTSEDAVEYFCRKSRY-----SHWGSGITLV 134
QY 121 SS-----GGGGGGGGGGGGGGSDIELTOSPSLAVSAGEKVMASCKSSOSLJNSRTR 173
D 135 SSGKTPPVGGGGGGGGGGGGGGSDIYWSOSPSPVSVGEKVLTSCKSSOSLJYSSNOK 194
QY 174 NYLAMYQOKPGQSPKVLLYMASTRESGVPDFTFTSGSGIDFTLLTSSVOAEDIALVAYYCK 233
D 195 NYLAMYQOKPGQSPKRLLYMASAESGVPDRFTSGSGIDFTLLTSSVKEMEDIALVAYYCCQ 254
QY 234 SYNLP-TRFGSGTKLEIK 249
D 255 YSYPLTFPGAGTKLVK 271

```

```

RESULT 11
US-09-594-985A-7
: Sequence 7, Application US/09594985A
: GENERAL INFORMATION:
: APPLICANT: Barbera-Guillem, Emilio
: APPLICANT: Nelson, M. Bud
: TITLE OF INVENTION: Vaccine formulations and methods for immunizing an
: FILE OF INVENTION: Individual against shed antigen-specific B cells
: FILE REFERENCE: B-25np
: CURRENT APPLICATION NUMBER: US/09/594,985A
: CURRENT FILING DATE: 2000-09-12
: PRIOR APPLICATION NUMBER: US 60/139,521
: PRIOR FILING DATE: 1999-06-16
: NUMBER OF SEQ. ID NOS: 21
: SOFTWARE: WordPerfect
: SEQ. ID NO. 7
: LENGTH: 272
: TYPE: PRT

```

```

; ORGANISM: Artificial sequence
;
; FEATURE:
;
; NAME/KEY:
;
; LOCATION:
;
; OTHER INFORMATION: synthesized
;
US-09-594-985A-7

```

Query Match	68.2%;	Score 896.5;	DB 19;	Length 272;
Best Local Similarity	66.7%;	Pred. No. 1.8e-71;		
Matches 172; Conservative	31;	Mismatches 38;	Indels 17;	Gaps 3

[illegible]

RESULT 12
 US-09-468-029-68
 Sequence 68, Application US/09468029
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: B7-Binding molecules for treating immune
 TITLE OF INVENTION: diseases.
 NUMBER OF SEQUENCES: 80
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/468,029
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP98/03791
 FILING DATE: *
 INFORMATION FOR SEQ ID NO: 68:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 268 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 US-09-468-029-68

Query Match	66.9%	Score 880;	DB 18;	Length 268;
Best Local Similarity	69.5%;	Pred. No. 5.1e-70;		
Matches 173;	Conservative 22;	Mismatches 44;	Indels 10;	Gaps 1

[illegible]

DB 83 NPKREGATLVKSSSTAVMOLESLTSEDSAVYYCARFAAYGDIYYIMDYGOGTIVTV 142
QY 121 SSGGGGGGGGGGGGSDIELTQSPSLAVSAGEKVMASCKSSOSLNSRTRKMYLAMYQ 180
DB 143 S-----SSGGGSDIELTQSPSLAVSAGEEVTWCKSSOSVLYSSNQKMYLAMYQ 192
QY 181 QKPGQSPKLYIWMASRESGVDPDRFTGSGGSDFTLTITSSVQAEADLAVYYCKOSYNLPTF 240
DB 193 QKPGQSPKLYIWMASRESGVDPDRFTGSGGSDFTLTITSSVQAEADLAVYYCHQYLSMTF 252
QY 241 GGGTKLEIK 249
DB 253 GGGTKLEIK 261

RESULT 13

US-09-364-088-16
; Sequence 16, Application US/09364088
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA: US 08/484,172
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-364-088-16

Query Match 66.7%; Score 877; DB 17; Length 553;
Best Local Similarity 66.5%; Pred. No. 2.4e-69;
Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

QY 2 VKLOESGAEIYVRGASVNSCTASGFNIRKDYMMWVKORPEEGLEWIGYIDPESGETEYA 61
DB 278 IKLOOSGAEIYVRGSGTSYKLSCTASGFNIRKDYMMWVKORPEEGLEWIGYIDPESGETEYA 337
QY 62 PNFQGRATVADTSSNTAVLHLSLTSEDTTYYYCNAVYYEYDG-----YALDIWGGGT 116
DB 338 PNFQGRATVADTSSNTAVLHLSLTSEDTTYYYCNAVYYCN-----EGPTGTGYIDWGGGT 390

QY 117 TVTVSSGGGGGGGGGGGSDIELTQSPSLAVSAGEKVMASCKSSOSLNSRTRKMYL 176
DB 391 TVTVSSGGGGGGGGGGGSENVLTQSPALMASGEEKYITCSASSSV-----SYM 443
QY 177 AMYQKPGQSPKLYIWMASRESGVDPDRFTGSGGSDFTLTITSSVQAEADLAVYYCKOSYN 236
DB 444 HMFQKPGTSFKMTYISTNSLASGVPARFSGSGGTSYSLTISRMEADATYYCCQRRS 503
QY 237 LP-TFEGGTKEIK 249
DB 504 YPLTFAGTKLEIK 517

RESULT 14

US-09-523-279-16
; Sequence 16, Application US/09523279
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISES OF ANTI-FC RECEPTOR
; TITLE OF INVENTION: BINDING AGENTS
; FILE REFERENCE: MXI-043CP3
; CURRENT APPLICATION NUMBER: US/09/523,279
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/364,088
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/188,082
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 08/661,052
; PRIOR FILING DATE: 1996-07-07
; PRIOR APPLICATION NUMBER: 08/484,172
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-523-279-16

Query Match 66.7%; Score 877; DB 19; Length 553;
Best Local Similarity 66.5%; Pred. No. 2.4e-69;
Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

QY 2 VKLOESGAEIYVRGASVNSCTASGFNIRKDYMMWVKORPEEGLEWIGYIDPESGETEYA 61
DB 278 IKLOOSGAEIYVRGSGTSYKLSCTASGFNIRKDYMMWVKORPEEGLEWIGYIDPESGETEYA 337
QY 62 PNFQGRATVADTSSNTAVLHLSLTSEDTTYYYCNAVYYEYDG-----YALDIWGGGT 116
DB 338 PNFQGRATVADTSSNTAVLHLSLTSEDTTYYYCNAVYYCN-----EGPTGTGYIDWGGGT 390
QY 117 TVTVSSGGGGGGGGGGGSDIELTQSPSLAVSAGEKVMASCKSSOSLNSRTRKMYL 176
DB 391 TVTVSSGGGGGGGGGGGSENVLTQSPALMASGEEKYITCSASSSV-----SYM 443
QY 177 AMYQKPGQSPKLYIWMASRESGVDPDRFTGSGGSDFTLTITSSVQAEADLAVYYCKOSYN 236
DB 444 HMFQKPGTSFKMTYISTNSLASGVPARFSGSGGTSYSLTISRMEADATYYCCQRRS 503
QY 237 LP-TFEGGTKEIK 249
DB 504 YPLTFAGTKLEIK 517

RESULT 15

US-09-188-082-16
; Sequence 16, Application US/09188082
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Cheilan Somasundaram

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-16

Query Match 66.7% Score 877; DB 27; Length 553;
Best Local Similarity 66.5% Pred. No. 2.4e-69;
Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

QY 2 VKLQSGAEIVRSASVNLCTASGFNIDYHWMVKRPEEGLEWIGYIDPESGETEYA 61
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QY 62 PNEQKATVTADTSSNTATLHSLTSEDTTYVCNAVITYEYD-----YALDIWGQGT 116
DB 338 PFOGKATFTTDTSSNTATLHSLTSEDTTYVCNAVITYEYD-----EGTPTGPFYFDYWGQGT 390
QY 117 TVTVSSGGGGGGGGGGGGSDIELTQSPSLAVSAGEVAMCKSSOSLFNSRTKNTL 176
DB 391 TVTVSSGGGGGGGGGGGGSDIELTQSPSLAVSAGEVAMCKSSOSLFNSRTKNTL 443
QY 177 AMYQKPGQSPKYLIVASTRESGVDPDRFTGSGSGTDFLTLLISSVOEDLAVYCKQSYN 236
DB 444 HMFQKPGQSPKYLIVASTRESGVDPDRFTGSGSGTDFLTLLISSVOEDLAVYCKQSYN 503
QY 237 LP-TFEGGKLEIK 249
DB 504 YPLTFGAGTKLEIK 517

Search completed: February 12, 2001, 15:26:22
Job time: 212 sec

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QY 481 aatcagtcagagctgttcaacagtagaacccgaagaattactgtgtgatacag 540
Db 463 AAGTCAGTCAGAGCCTTTGGA---TAGTATGAGAAAAACATATTGAAATGGTTA 519
QY 541 cagaaccagagcagctctcctaagagtcgtatctactgtgacatccactaggaatctga 600
Db 520 CAGAGCCAGAGCCAGTCTCCAAAGCGCTATCTATCTGTGCTTAACAGACTCTGGA 579
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Db 700 TTGCGTGTGCGACCAAGCTGGAATTAA 729

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RESULT 15
LOCUS A57272 768 bp DNA PAT 03-MAR-1998
DEFINITION Sequence 4 from Patent WO9630512.
ACCESSION A57272 GI:3713167
VERSION A57272.1 GI:3713167
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 768)
AUTHORS Bracco, U., Schweighofer, F. and Tocque, B.
TITLE CONDITIONAL EXPRESSION SYSTEM
JOURNAL Patent: WO 9630512-A 4 03-OCT-1996;
Rhone-Poulenc Rorer SA (FR)
COMMENT Other publication AU 5402096 961016
Other publication FR 2732348 961004.
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BASE COUNT 181 a 185 c 218 g 184 t
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QY 121 ccctgaagagcctgagtgatgtgatatctgactcctgaagtggtgaactgaatat 180
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QY 181 gccctgaacttcagagcagagccactgtgactgcagacacatctccacacagctac 240
Db 208 GCCCCGAGATTCCAGGCGCAGGCGCAGCATATGACAGACACATCTCCATACAGCTAC 267
QY 241 ctgcacctcagagcctgagatctgagagacacacagctctattactgttaatgcagtc 300
Db 268 CTGCAGCTCAGCAGCTGCGATCTGAGGACACTGCCGTGATATTGTAAAT----- 318

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QY 301 tactatgaatcagacggtatcttltgactacttggggcgaaggacacagtcacgctc 360
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QY 361 tctctagtgagggcggttctcagagcagagtggtctctggcggtgggggtcagacttg 420
Db 370 TCTCTAGGTGAGGCGGCTCAGGCGGAGGTGCTCTGGCGGTGGGATCGGATGTTTG 429
QY 421 ccaaccagctccactcttccctgtgtgtcagcagagagaagtgctgtgactgctgc 480
Db 430 ATGACCCAACTCCACTCTTGTGCTTACATTGGACAAACACACCTCCACTCTTGC 489
QY 481 aatcagtcagagctgttcaacagtagaacccgaagaattactgtgtgatacag 540
Db 490 AAGTCAGTCAGAGCCTTTGGA---TAGTATGAGAAAAACATATTGAAATGGTTA 546
QY 541 cagaaccagagcagctctcctaagagtcgtatctactgtgacatccactaggaatctga 600
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QY 601 gtccctgacgttcaacagcagtagatctggagacagatttcaactctaccatcagcagt 660
Db 607 GTCCCTGACAGTTCACACTGCGACTGATCAGGACAGATTTTCACTTAAATCAACAGA 666
QY 661 gtccagctcgaagactgtgagttatctactgtcgaagcaa---tctataatctaccagag 717
Db 667 GTGAGGCTGAGGATTGGAGTTATATTGCTGCGAAGTACACATCTCCGCTTACG 726
QY 718 ttccgctgggagcacaagctggaatcaaa 747
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 Job time: 35041 sec

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 Db 127 CCGTAACAGGCGCTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 186
 QY 181 gccccaactctcagagcagagcagcctgctgactgacagacacacccctccacagacctac 240
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 Db 187 GCCCCGAAGTTCAGAGGCAAGGCCACTATACCTGACAGACACTCTCCATTAACAGCTTAC 246
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 LOCUS AC0131532
 DEFINITION Synthetic construct for anti-p53 ScFv antibody (scfv421) containing linker sequence.
 ACCESSION AJ131532
 VERSION AJ131532.1 GI:4033863
 KEYWORDS antibody; immunoglobulin superfamily; ScFv; variable region.
 SOURCE Synthetic construct.
 ORGANISM Artificial construct.
 REFERENCE 1 (bases 1 to 729)
 AUTHORS Caron de Fromental, C., Gruel, N., Venot, C., Debussche, L.,
 Resurrection of transcriptional activity of p53 mutants in human
 tumour cells by intracellular expression of anti-p53 single chain
 Fv fragments
 TITLE
 JOURNAL Oncogene 18 (2), 551-557 (1999)
 MEDLINE 99124402
 REFERENCE 2 (bases 1 to 729)
 AUTHORS de Fromental, C.
 TITLE Direct Submission
 JOURNAL Submitted (16-DEC-1998) de Fromental C., U 380 INSERM, Institut

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 Cochin de Genetique Molculaire, 22 rue Mechain PARIS, 75014, FRANCE
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 LDSDEKTYLNMILQPGQSPRLIYLSKLSGVPDRFTGSGSGTDFLKINRYEAD
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 QY 241 ctgacacctcagcagcctgacatctgagagacacacacgctctactactgtaagcagtcac 300
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RESULT 10
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LOCUS Sequence 66 from Patent WO925818.
DEFINITION AX003772
ACCESSION AX003772.1 GI:9925753
VERSION
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 744)
AUTHORS Kufer, P. and Raum, T.
TITLE Method of identifying binding site domains that retain the capacity
of binding to an epitope
JOURNAL Patent: WO 9925818-A 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
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Matches 585; Conservative 0; Mismatches 145; Indels 12; Gaps 2;
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QY 69 agcttcgtctcaactcaactatactatactgacactggtgtaaacagggccctga 128
Db 72 GGGTTCTGATGAGCTGCTTCACTACTAGCTGGCTGGTTAAGCAGAGGCTTGACA 131
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QY 189 ctccagggcagagctgctgacacacacacacacacacacacacacacacacacac 248
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QY 429 gttccatcttccctgctgctgctcagcagagagagagagagagagagagagagag 488
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QY 489 tcagagtcgttcaacagtagaacccgaagaattactggtctgtgtatcagaagaacc 548
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QY 549 agggcagcttcctaaagtctgatactactcagagagagagagagagagagagagagag 608
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QY 609 tcgcttcacagcagtgatctgagacagattcaactcaccatcagaagtgtaggc 668
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Db 723 GGGACCAAGCTTGAGATCAAA 744
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AX003780 744 bp DNA ROD 24-AUG-2000
LOCUS Sequence 74 from Patent WO925818.
DEFINITION AX003780
ACCESSION AX003780
VERSION AX003780.1 GI:9925757
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 744)
AUTHORS Kufer, P. and Raum, T.
TITLE Method of identifying binding site domains that retain the capacity
of binding to an epitope
JOURNAL Patent: WO 9925818-A 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES
source
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Best Local Similarity 78.6%; Pred. No. 6.7e-125;
Matches 583; Conservative 0; Mismatches 147; Indels 12; Gaps 2;
QY 9 gctcagagtgtaaggcagaactgtgagtcaggggccctcaactgttctctgac 68
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QY 69 agcttcgtctcaactcaactatactatactgacactggtgtaaacagagggccctga 128
Db 72 GGGTTCTGATGAGCTGCTTCACTACTAGCTGGCTGGTTAAGCAGAGGCTTGACA 131
QY 129 gggccgagagtgattgataatgatactcctgagtggtgtaactgataatgccccga 188
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RESULT 7
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LOCUS
DEFINITION Sequence 59 from Patent WO9858965.
ACCESSION AX001511
VERSION AX001511.1 GI:7241663
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1668)
AUTHORS Bosman, A. and Lorre, K.
TITLE B7-BINDING MOLECULES FOR TREATING IMMUNE DISEASES
JOURNAL Patent: WO 9858965-A 30-DEC-1998;
BOSMAN ALFONS (BE); LORE KATHRIEN (BE)
LOCATION/Qualifiers

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BASE COUNT 409 a 424 c 453 g 382 t
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Best Local Similarity 79.9%; Pred. No. 2,8e-136;
Matches 591; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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QY 68 cagcttcgtgctcaaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaatcaat 127
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QY 128 agggccctgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 187
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QY 368 gtagcag 427
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RESULT 8
XX031739 864 bp DNA SYN 05-SEP-1995
LOCUS
DEFINITION Single chain antibody SCA 13.1 gene, complete cds.
ACCESSION U31739
VERSION U31739.1 GI:975304
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 864)
AUTHORS Nardone, F., Spano, F. and Crisanti, A.
TITLE Direct Submission
JOURNAL Submitted (17-JUL-1995) Francesco Nardone, Istituto di
Parassitologia, University of Rome 'La Sapienza', Piazzale Aldo
Moro 5, Roma, RM 00185, Italy
LOCATION/Qualifiers

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/note="encodes CDR 2"

misc_feature 361..393
/note="encodes CDR 3"

misc_feature 427..471
/note="encodes linker peptide"

misc_feature 472..810
/note="variable region from light chain"

misc_feature 541..588
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/note="encodes CDR 2"

misc_feature 751..774
/note="encodes CDR 3"

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BASE COUNT 205 a 222 c 234 g 203 t
ORIGIN

Query Match 63.1%; Score 471; DB 12; Length 864;


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OY 661 gtccagcgttaaacctgagcttattactgaagcaatctataatctaccagcttc 720
Db 715 GTCCAGGCTGAACCTGGCAATTATTACTGAGCAATCTATTACTCTCGGAGCTTC 774
OY 721 ggcgggggacccaagctggaataca 747
Db 775 GGTGAGGCGCACCAAGCTCGAGATCAAA 801

RESULT 4
A83217 2025 bp DNA PAT 21-JAN-2000
LOCUS A83217 Sequence 37 from Patent WO9851787.
DEFINITION A83217
ACCESSION A83217
VERSION A83217.1 GI:6732659
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2025)
AUTHORS Emery, S.C. and Blakey, D.C.
TITLE CHEMICAL COMPOUNDS
JOURNAL Patent: WO 9851787-A 19-NOV-1998;
EMERY STEPHEN CHARLES (GB); ZENECA LTD (GB)
FEATURES
source 1. 2025
/organism="unidentified"
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BASE COUNT 440 a 604 c 638 g 343 t
ORIGIN

Query Match 73.4%; Score 548.6; DB 81; Length 2025;
Best Local Similarity 84.3%; Pred. No. 4,5e-150;
Matches 630; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

OY 1 caagtcagctgagcagagtcagagcagaaactgtgagtcagggcctcagcattg 60
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Db 118 TCCTGCAAGGCTTCTGCTACACCTTCACCGGCTACTGATACACTGGTGAAGCAGAGG 177
OY 121 ccggaagagggcgtgagtgatgatataatgatcgcgtgagtggtgaactaatat 180
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Db 238 AATGAGAGTTCAGAAACAAGGCGCACACTGACTGATGACAAATCTCCACACAGCCTAC 297
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OY 541 cagaaccagagcagcttctcctaagtgctgactactatggcattcactagaggaaatgga 600
Db 595 CAGAGACGAGGCGAGTCTCTAACTGATCTATGCGGCTACCTAGGACATCTGGG 654
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Db 655 GTCCCTGATCGCTTCACAGGCACTGATGGAGATTCTACTCTCACATCAGCAGT 714
OY 661 gtccagcgttaaacctgagcttattactgaagcaatctataatctaccagcttc 720
Db 715 GTCCAGGCTGAACCTGGCAATTATTACTGAGCAATCTATTACTCTCGGAGCTTC 774
OY 721 ggcgggggacccaagctggaataca 747
Db 775 GGTGAGGCGCACCAAGCTCGAGATCAAA 801

RESULT 5
MMU131195 786 bp mRNA ROD 07-JAN-1999
LOCUS MMU131195 Mus musculus mRNA for single chain antibody scfv.
DEFINITION AJ131195
ACCESSION AJ131195
VERSION AJ131195.1 GI:4138226
KEYWORDS ILB6scfv gene; antibody; scfv; single chain antibody.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 786)
AUTHORS Rodentia; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Bremaud, L., Pellissier, P., Tellaud, J.L., Kadenbach, B., Cogne, M. and
Ratnaud, M.H.
JOURNAL Molecular cloning, expression and characterization of a functional
single chain immunoglobulin variable fragment (scfv) to the
nuclear-encoded subunits Viac of mammalian cytochrome c oxidase
unpublished
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source Location/Qualifiers
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32	407	54.5	789	13	AF001527
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36	400.6	53.6	3970	12	AS214585
37	400.6	53.6	4363	12	SCFV18280
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39	400	53.5	756	81	A76868
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					AR088013 Sequence 8
					AF6021 Sequence 3
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					Z29460 M.musculus
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ALIGNMENTS

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RESULT 1
AC0131533
LOCUS          AC0131533      747 bp      mRNA          SYN          16-MAR-2000
DEFINITION     Synthetic construct for anti-p53 scFv antibody (scFv1D3)
                containing linker sequence.
ACCESSION      AJ131533
VERSION        AJ131533.1  GI:4033867
KEYWORDS       antibody; immunoglobulin superfamily; scFv; variable region.
SOURCE         ORGANISM
                artificial construct.
                synthetic construct.
REFERENCE      1 (bases 1 to 747)
                Caton de Fromental,C., Gruel,N., Venot,C., Debussche,L.,
                Consellier,E., Dureau,C., Tellaud,J.L., Tocque,B. and Bracco,L.
                Restoration of transcriptional activity of p53 mutants in human
                tumour cells by intracellular expression of anti-p53 single chain
                Fv fragments
JOURNAL        Oncogene 18 (2), 551-557 (1999)
MEDLINE        99124402
REFERENCE      2 (bases 1 to 747)
                de Fromental,C.
TITLE          Direct Submission
                Submitted (16-DEC-1998) de Fromental C., U 380 INSERM, Institut
                Cochin de Genetique Moleculaire, 22 rue Mechain PARIS, 75014,
                FRANCE
FEATURES
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[illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 22:57:49 ; Search time 1856.43 Seconds
(without alignments)
2059.307 Million cell updates/sec

Title: US-09-297-181-3

Perfect score: 747
Sequence: 1 caggtcaagctgcagaggtc.....gcaccaagctggaatcaaa 747

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	747	100.0	747	12 ACO131533	AJ131533 Synthetic
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4	548.6	73.4	2025	81 A83217	A83217 Sequence 37
5	514.4	68.3	786	11 MMU131195	AJ131195 Mus muscu
6	510.2	68.3	1725	13 AX001509	AX001509 Sequence
7	501.6	67.1	1668	13 AX001511	AX001511 Sequence
8	471	63.1	864	12 XXU1739	U31739 Single chr
9	469.2	62.8	4354	12 ASY14583	Y14583 Artificial
10	466	62.4	744	11 AX003772	AX003772 Sequence
11	462.8	62.0	744	11 AX003780	AX003780 Sequence
12	457.6	61.3	749	81 A59386	A59386 Sequence 36
13	457.6	61.3	1611	81 A59381	A59381 Sequence 31
14	454.4	60.3	729	12 ACO131532	AJ131532 Synthetic
15	452.8	60.5	768	81 A57272	A57272 Sequence 4
16	448.4	60.0	744	11 AX003782	AX003782 Sequence
17	447.8	59.3	723	12 AF169027	AF169027 Synthetic
18	446	59.7	1314	81 A68604	A68604 Sequence 1
19	442.4	59.2	810	81 A45006	A45006 Sequence 1
20	438.4	58.7	1679	81 AR054409	AR054409 Sequence
21	435.4	58.3	804	13 AX001519	AX001519 Sequence

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Db 444 HMEQKPGTSPKLMYSTNSLAGVPARFSGSGSTSYSLTISRMEADATYYCOORSS 503
QY 237 LP-TFGGGTKLEIK 249
Db 504 YPLTFGAGTKLEIK 517

RESULT 4

US-08-797-689-18
Sequence 18, Application US/08797689
Patent No. 5876969
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Yeh, Patricia
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
CLASSIFICATION: 435
FILING DATE: 31-JAN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-797-689-18

Query Match 64.1%; Score 842.5; DB 2; Length 249;
Best Local Similarity 64.6%; Pred. No. 1.7e-63;
Matches 164; Conservative 39; Mismatches 38; Indels 13; Gaps 4;
QY 1 QVLOESGAEVLVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGYIDPESGTEV 60
Db 4 QVLESGPELVVPGASVYISKASGYAFGRSMNMWKORPGGLEIGRITGYDGDGTIX 63
QY 61 APNFOGKAITYTADTSSNTAVILHLSLTSEDTYYIC---NAVYYIYDGYALDYWGQGT 116
Db 64 NGFKGKATLADRSSSTAYMOLSLTSGSAVYFCAKENNR--FDRGYYADYWGQGT 121

QY 117 TVTVSSGGGGGGGGGGGGSDIELTQSPSLAVSAGEKRVAMCKSKQSGLFNSRTKRYL 176
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QY 177 AMYQKPGQSPKLYIMASTRESGVDPRTGSGSGTDFLLTSSVQAEADLANYICKQSTN 236
Db 176 AMYQKPGQSPKLYIMASTRHTGYDPRTGSGSGTDFLLTSSVQSEDSADYFCQOYSS 235
QY 237 LP-TFGGGTKLEIK 249
Db 236 YPWTFGGGTKLEIK 249

RESULT 5

US-08-256-790-2
Sequence 2, Application US/08256790
Patent No. 5910573
GENERAL INFORMATION:
APPLICANT: PLUECKTHUN, ANDREAS
APPLICANT: PACK, PETER
TITLE OF INVENTION: MONOMERIC AND DIMERIC ANTIBODY FRAGMENT
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILDEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,790
FILING DATE: 22-JUL-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00082
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92101069
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1598
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-790-2

Query Match 63.2%; Score 831.5; DB 2; Length 277;
Best Local Similarity 65.5%; Pred. No. 1.6e-62;
Matches 165; Conservative 29; Mismatches 53; Indels 5; Gaps 4;
QY 1 QVLOESGAEVLVSGASVNLCTASGFNIKDYMHVWKORPEGLMIGYIDPESGE--T 58
Db 22 EVLVSSGGGGLVPGASVYISKASGYAFGRSMNMWKORPGGLEIGRITGYDGDGTIX 81
QY 59 EYAPNFOGKAITYTADTSSNTAVILHLSLTSEDTYYICNAVYYIYDGYALDYWGQGT 118
Db 82 EYASVYKGRFIVSRDTSOSILYQNNALRAEDTAIYIC-ARNYYGSTW-FDVGAGTIV 139

QY 119 TVSSGGGGGGGGGGGGSDIELTQSPSSLA VSA G E K V A M S C K S S O G L F N S R T R K N Y L A W 178
140 TVSSGGGGGGGGGGGGSDI V M T Q S P S S L V S A G E H V T M S C K S S O G L F N S R T R K N Y L A W 199
QY 179 YQKPGSPKVLIIYMASTRSGVDPDRFTGSGSGDTFTLTSSVQAEDLAVYYCKQSYNLP 238
200 YQKPGSPKVLIIYMASTRSGVDPDRFTGSGSGDTFTLTSSVQAEDLAVYYCKQSYNLP 259
QY 239 -TFGGGTKEIK 249
260 LTFGAGTKLEIK 271

RESULT 6
US-08-553-497A-20
Sequence 20, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSEW, DETLEF
APPLICANT: ADAM, JAUDE
APPLICANT: MITTANS, FRANCES
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PILATS, JAUDE
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: NO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-20

Query Match 62.6% Score 823.5; DB 2; Length 244;
Best Local Similarity 63.1%; Pred. No. 6, 5e-62;

Matches 159; Conservative 33; Mismatches 49; Indels 11; Gaps 3;
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1 EVQLOQSGAEIYVPGASVNLCTASGFNIDYVNMHWKQRPPEGLMIGYIDPESETEX 60
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61 NEKFKSKATLVYDKSSSTAMQLSLTSEDSAVYYC-ASRDYDYDGRYEDYWGQGTIVY 119
QY 121 SSGGGGGGGGGGGGGSDIELTQSPSSLA VSA G E K V A M S C K S S O G L F N S R T R K N Y L A W 180
120 SSGGGGGGGGGGGGGSDIELTQSPSSLA VSA G E K V A M S C K S S O G L F N S R T R K N Y L A W 172
QY 181 QKPGSPKVLIIYMASTRSGVDPDRFTGSGSGDTFTLTSSVQAEDLAVYYCKQSYNLP 238
173 QKPGSPKVLIIYMASTRSGVDPDRFTGSGSGDTFTLTSSVQAEDLAVYYCKQSYNLP 222
QY 239 -TFGGGTKEIK 249
233 YTFGGGTKEIK 244

RESULT 7
US-08-661-052-14
Sequence 14, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Robert Goldstein
APPLICANT: Robert Graziano
APPLICANT: Cheilan Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LARIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-14

Query Match 62.2% Score 818; DB 2; Length 301;
Best Local Similarity 62.1%; Pred. No. 2, 4e-61;
Matches 154; Conservative 37; Mismatches 35; Indels 2; Gaps 2;

DY 2 VKLDSEGLVRSASAVSLSTAGSGFNKDYMMHVKORPEEGLEWTCGDIPEGGEFEYA 6

Db 21 IQLVESGGGVQPPGRSRLRCLSCSSCGFFISDNYMTWKQAPKGKGLEWATTSDDGSYYTP 80

OY 62 PNFQAKATVTADTSSNTAYHLSELTSBEDTVVXYXCNAYIYEYDGVALDWGQGCTIVVS 121
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.

Db 81 DSVAGRFTISDNKNLTLFLQMDSLREDTGVCYC-ARGYRYRG-AMDYWGOGTPTYS 138

OY 122 SGGGGGGGGGGGGGSDIELTOFSPSSLVASGAEKVAMSKSSOSLFNSRTFRKNLYAQO 181
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 139 SGGGGSGGGGGGGGDIDLQTQSPPSSLSASVGDEHTVITCKSQSVLSSNQKNLYAQO 198

OY 182 KPGSGPKLIYWASTRESGVDFDRFGSGSGDFELTTISSVAEDLAYYYOKSNLPFG 244
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 199 KPGNAPKLLIWASTRESGVPSRFSGSGSDTFFTLTSSLOPEDIAITYCHQILDSWFTE 258

OY 242 GGTKEIK 249
|||:||||

Db 259 QGTKEYEK 266

RESULT 8
US-08-553-497A-26
Sequence 26, Application US/08553497A
Patent No. 5844093

GENERAL INFORMATION:
APPLICANT: KETTERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCESC
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCOC, FRANCESCO
APPLICANT: PIJATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 26:
LENGTH: 242 amino acids

```

: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: Protein
US-08-553-497A-26

Query Match 61.9%: Score 813.5; DB 2: Length 242;
Best Local Similarity 64.0%: Pred. No. 4,4e-61;
Matches 160; Conservative 28; Mismatches 53; Indels 9; Gaps 3

QY 1 QVKLDESGAEELVRSASVNLCTAGFNLKDYMMHWVKORPEEGLEWIGYIDPESGETEX 60
DB 1 QVKLOESGAEELYKPKASVKLSCKRAGCYPTSMHMMHWKORAGGLEWIEINRTPATY 60
QY 61 APNFOGKATVADITSSNTAYLHLSLTSEDITVYCNNAVITYEYDVALDWGGTTVTV 120
DB 61 NEKFSKSKATLIVDKSSSTAYMQLSSLTSEDSAVYCC-ASRDYDDGRYFDYWGQTTVTV 119
QY 121 SSGGGSGSGSGSGSGGSPDIELTQSPSSSLAVSAGEKVMASCKSSQSLFNSRFRKNYLA 180
DB 120 SSGGGSGSGSGSGSGGSDIELTQSPITMSASPGKVTMTCSOSSV-----SYTWYQ 172
QY 181 QKPGSPYLVITWASTRSGVDPDRFTGSSGSDFTLTITSSVOAEDLAVYCKOSYMLP-T 239
DB 173 QKTGSPFLITDITNLSAGVYPRFSGSGSISYSLTISRMRADPATYTCQWSSYPLT 232
QY 240 FGGGTKEIK 249
DB 233 FGGGTKEIK 242

RESULT 9
US-08-553-497A-24
: Sequence 24, Application US/08553497A
: Patent No. 5844093
: GENERAL INFORMATION:
: APPLICANT: KETLEBOROUGH, C. A.
: APPLICANT: BENDIG, MARY M.
: APPLICANT: ANSELL, KEITH H.
: APPLICANT: GUSSOW, DETLEF
: APPLICANT: ADAM, JAUME
: APPLICANT: MITTANS, FRANCES
: APPLICANT: ROSELL, ELISABET
: APPLICANT: BLASCO, FRANCESC
: APPLICANT: PUJOLTS, JAUME
: TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
: TITLE OF INVENTION: ANTIBODIES
: NUMBER OF SEQUENCES: 30
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
: STREET: 2200 CLARENDON BLVD. SUITE 1400
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: US
: ZIP: 22201
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/553,497A
: FILING DATE: 17-NOV-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/EP95/00978
: FILING DATE: 16-MAR-1995
: PRIOR APPLICATION NUMBER: EP 94104160.0
: FILING DATE: 17-MAR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EP 94118970.6
: FILING DATE: 02-DEC-1994

```

RESULT 11
US-08-392-338A-19
Sequence 19, Application US/08392338A
Patent NO. 5863620
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
;; STREET: 1100 New York Avenue, NW
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/166,093
;; FILING DATE: Herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/392,338
;; FILING DATE: 22-FEB-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/989,846
;; FILING DATE: 20-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/796,936
;; FILING DATE: 25-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldstein, Jorge A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.003000B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2540
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 483 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-166-093-19

Query Match 61.1%; Score 803.5; DB 3; Length 483;
Best Local Similarity 62.4%; Pred. No. 7.1e-60;
Matches 156; Conservative 32; Mismatches 39; Indels 23; Gaps 3;

QY 1 QVQLQESGAEIVSGASVNLCTASGFNIDYMHVMWKORPEGLMIGYIDPESGETEV 60
DB 128 QVQLQSDALIVKPGASVSKCAAGITFDHAIHWKONPEGLMIGYIFSGNDDFKY 187
QY 61 APNFOGKATVADTSSNTAYLHLSLTSEDITYYCNNAVITYEYDGYALDYWGQGTIVY 120
DB 188 NERFKKATLTADKSSSTAYVOLNLSLSEDSAVYFCTRSL-----NMAVWGQGTIVY 240
QY 121 SSGGGGSGGGGGGSDILTOSPSLAVSAGEKVMKSKSSQSLNSKTRKNYLAWYQ 180
DB 241 S-----SDVVMSSPSSLPVSGEKVTLCKSSQSLLYSGNKNYLAWYQ 285
QY 181 QKPGSPKVLIVYASTRESGVPRFTGSGSGDTFTLTISVQAEADLAVYYCKOSYNLP-T 239
DB 286 QKPGSPKVLIVYASARESEVPRFTGSGSGDTFTLTISVSKIEDLAVYYCCQYISYPLT 345
QY 240 FGGGTKLEIK 249
DB 346 FGAGTKLVK 355

RESULT 14
US-09-172-019-19
; Sequence 19, Application US/09172019
; Patent No. 6103889
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Hardman, Karl

;; APPLICANT: Bird, Robert
;; APPLICANT: Filipula, David
;; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
;; TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
;; STREET: 1100 New York Avenue, NW
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/172,019
;; FILING DATE: Herewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/392,338
;; FILING DATE: 22-FEB-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/989,846
;; FILING DATE: 20-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/796,936
;; FILING DATE: 25-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Goldstein, Jorge A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 0977.003000D
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 483 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-172-019-19

Query Match 61.1%; Score 803.5; DB 3; Length 483;
Best Local Similarity 62.4%; Pred. No. 7.1e-60;
Matches 156; Conservative 32; Mismatches 39; Indels 23; Gaps 3;

QY 1 QVQLQESGAEIVSGASVNLCTASGFNIDYMHVMWKORPEGLMIGYIDPESGETEV 60
DB 128 QVQLQSDALIVKPGASVSKCAAGITFDHAIHWKONPEGLMIGYIFSGNDDFKY 187
QY 61 APNFOGKATVADTSSNTAYLHLSLTSEDITYYCNNAVITYEYDGYALDYWGQGTIVY 120
DB 188 NERFKKATLTADKSSSTAYVOLNLSLSEDSAVYFCTRSL-----NMAVWGQGTIVY 240
QY 121 SSGGGGSGGGGGGSDILTOSPSLAVSAGEKVMKSKSSQSLNSKTRKNYLAWYQ 180
DB 241 S-----SDVVMSSPSSLPVSGEKVTLCKSSQSLLYSGNKNYLAWYQ 285
QY 181 QKPGSPKVLIVYASTRESGVPRFTGSGSGDTFTLTISVQAEADLAVYYCKOSYNLP-T 239
DB 286 QKPGSPKVLIVYASARESEVPRFTGSGSGDTFTLTISVSKIEDLAVYYCCQYISYPLT 345
QY 240 FGGGTKLEIK 249
DB 346 FGAGTKLVK 355

RESULT 15
US-09-166-094-19

Sequence 19, Application US/09166094
Patent No. 6121424
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/166,094
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-166-094-19

Query Match 61.1%; Score 803.5; DB 3; Length 483;
Best Local Similarity 62.4%; Pred. No. 7.1e-60;
Matches 156; Conservative 32; Mismatches 39; Indels 23; Gaps 3;

QY 1 OYKLOESGAELVRSASVNLSCASGFNFKDYMHVVKORPEGLMIGYIDPESETEX 60
DB 128 OYOLQSDALVPGASVSKASGTTTDRHIVHVKORPEGLMIGYIDPESETEX 187
QY 61 APNFOGKATVADTSSNTAYLHLSTLSEDTVYVCNAVYYEYDGYALDYWGQGTTVY 120
DB 188 NERFRKATLTADKSSSTAYVQLNLSLSEDSAYVFCRSL-----NNAVWGQGTSTVY 240
QY 121 SSGGGSGGGGGSDIELTOSPPSLAVSAGEKYAMSGCKSSQSLFNSRTRKNYLAHQ 180
DB 241 S-----SDVYMSQSPSSLIPYSVEKYTLSCSKSSQSLYSGNCKNYLAHQ 285
QY 181 OKPGOSPXYLIWASTREGSVPRFTGSGSGTDFTLTSSVOAEDLAVYCKOSYLP-T 239
DB 286 OKPGOSPXYLIWASTREGSVPRFTGSGSGTDFTLTSSVOAEDLAVYCKOSYLP-L 345
QY 240 FGGGTLEIK 249

DB 346 FGGGTLEIK 355

Search completed: February 12, 2001, 15:23:46
Job time: 60 sec

5-40 00 000

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 23:01:10 : Search time 96.92 Seconds
(without alignments)
2895.378 Million cell updates/sec

Title: US-09-297-181-3
Perfect score: 747
Sequence: 1 caggtcaagctgcagagtc.....gcaccaagctgaaatcaaa 747

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18783343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 11: /cgn2_2/gcgdata/geneseq/geneseq/NA1990.DAT:*
- 12: /cgn2_2/gcgdata/geneseq/geneseq/NA1991.DAT:*
- 13: /cgn2_2/gcgdata/geneseq/geneseq/NA1992.DAT:*
- 14: /cgn2_2/gcgdata/geneseq/geneseq/NA1993.DAT:*
- 15: /cgn2_2/gcgdata/geneseq/geneseq/NA1994.DAT:*
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- 18: /cgn2_2/gcgdata/geneseq/geneseq/NA1997.DAT:*
- 19: /cgn2_2/gcgdata/geneseq/geneseq/NA1998.DAT:*
- 20: /cgn2_2/gcgdata/geneseq/geneseq/NA1999.DAT:*
- 21: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	747	100.0	747	19	V36237 DNA od ScFv D3M wh
2	548.6	73.4	864	20	V72072 Fusion protein PIC
3	548.6	73.4	2019	20	V72059 Plasmid pNG4/55.1s
4	548.6	73.4	2025	20	V72064 Fusion protein PNG
5	510.2	68.3	1725	20	X01651 Bispecific tetrava
6	504	67.5	759	19	V10378 Anti-CD86 monoclon
7	501.6	67.1	1668	20	X01652 Bispecific tetrava
8	466	62.4	744	20	X77243 Mouse scFv fragmen
9	462.8	62.0	744	20	X77247 Mouse scFv fragmen
10	460.8	61.7	729	19	V36236 DNA of ScFv 421 wh
11	457.6	61.3	749	18	T86234 Anti-human protein
12	457.6	61.3	1611	18	T86221 Human p53 protein

13	452.8	60.6	768	17	T48000
14	448.4	60.0	744	20	X77248
15	446	59.7	1314	19	V09256
16	442.4	59.2	810	16	Q90663
17	438.4	58.7	1679	18	T58150
18	438.4	58.7	1679	18	V08176
19	435.4	58.3	804	20	X01656
20	428.6	57.4	843	20	V72069
21	428.6	57.4	1998	20	V72075
22	428	57.3	748	21	Z28962
23	424	56.8	924	18	T94609
24	424	56.8	924	18	T66146
25	424	56.8	930	18	T94587
26	422.2	56.5	744	19	V11399
27	407	54.5	789	20	X01660
28	397.4	53.2	729	20	Z19786
29	397.4	53.2	729	20	Z07810
30	397.4	53.2	1467	20	V80292
31	397.4	53.2	1807	20	V80291
32	395.8	53.0	729	20	V80290
33	394.2	52.8	1518	20	V80294
34	394.2	52.8	2090	20	V80295
35	375.4	50.3	2165	15	Q68659
36	375.4	50.3	2165	15	Q68660
37	375.4	50.3	2165	15	X25408
38	375.4	50.3	2165	20	X25409
39	375.4	50.3	2165	20	X15395
40	375.4	50.3	2165	20	X15396
41	373.8	50.0	726	16	T04025
42	370.6	49.6	753	20	X77245
43	370.6	49.6	1637	21	Z88358
44	369.4	49.5	732	16	T04020
45	368.8	49.4	2478	20	X86614

ALIGNMENTS

RESULT 1	
V36237	
ID V36237 standard; DNA: 747 BP.	
XX V36237:	
AC	
XX	
XX	
DT 08-SEP-1998 (first entry)	
XX	
DE DNA od ScFv D3M which binds to mutant p53 proteins.	
XX	
XX Single chain antibody; ScFv D3M; mouse; p53 protein; oligomerisation;	
KW regulatory domain; p53 mutant; H273; W248; G281;	
KW p53-dependent trans-activating activity; restoration;	
KW tumour-suppressing activity; tumour cell; treatment;	
KW hyper-proliferation; cancer; re-stenosis; ss.	
OS Mus sp.	
XX	
XX W09818825-A1.	
PN	
PD 07-MAY-1998.	
XX	
XX 27-OCT-1997; 97WO-FR01921.	
PF	
XX 29-OCT-1996; 96FR-0013176.	
PR	
XX (RHON) RHONE-POULENC RORER SA.	
PA	
XX Debussche L, Bracco L;	
PI	
XX WPI: 1998-272143/24.	
DR P-PSDB; W60770.	
XX	
DR Restoring p53-dependent trans-activating activity to cell containing	
XX mutant p53 - by delivering single-chain antibody specific for the	
PT	

Coding sequence
Mouse scFv fragmen
Nucleotide sequenc
MFE-23 antibody co
Single chain anti-
H22-anti-CEA anti-
Anti-B7.2 monosp
Fusion protein PIC
Fusion protein (80
Human anti-glycoph
HindIII-EcoRI inse
scFv.4715-myc inse
EcoRI-HindIII inse
Human CD30 binding
Anti-B7.2 monosp
Anti-5T4 secreted
5T4 scFv antibody
Human B7-1.5T4.1 g
Anti-5T4 single ch
Murine anti-5T4 an
B7-1/scFv specific
scFv-IgE1 fusion c
CC49 VL-L-VH-L-VL-
CC49 VL-L-VH-L-VH-
CC49 single chain
DNA encoding a mul
DNA encoding a mul
Anti-BGR single c
Mouse scFv fragmen
Bispecific anti-ze
Anti-BGR single c
cDNA encoding an a

PT mutant, particularly for treatment of tumours
 XX
 PS Claim 5; Page 32; 54pp; French.

CC The present sequence encodes a single chain antibody (scFv) designated
 CC DJM. The antibody binds to an epitope present in the C-terminal region
 CC of the p53 protein that includes oligomerisation and regulatory domains,
 CC specifically between positions 320 and 393. scFv DJM is directed against
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the scFv is
 CC introduced into cells containing a mutant p53 protein, p53-dependent
 CC trans-activating activity is restored. scFv DJM is specific for
 CC p53-mutants that have lost tumour-suppressing activity and are present in
 CC tumour cells. It is particularly used to treat hyper-proliferation
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant
 CC and to purify or detect p53.

SQ Sequence 747 BP; 189 A; 188 C; 205 G; 165 T; 0 other;

Query Match 100.0%; Score 747; DB 19; Length 747;
 Best Local Similarity 100.0%; Pred. No. 3.1e-185;
 Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caggtcaagctgcaggaagtcaggagcagaactgtgagtcaggagccctcaatttg 60
 |||||
 DB 1 caggtcaagctgcaggaagtcaggagcagaactgtgagtcaggagccctcaatttg 60
 QY 61 tctctgcagagcttctggtctcaacataaagatactatgacatgggtggaacagagg 120
 |||||
 DB 61 tctctgcagagcttctggtctcaacataaagatactatgacatgggtggaacagagg 120
 QY 121 cctgaagagagcgtgagtgatgtgatctatgacatcctgaagagtggtgaacatgaat 180
 |||||
 DB 121 cctgaagagagcgtgagtgatgtgatctatgacatcctgaagagtggtgaacatgaat 180
 QY 181 gccccgaacttcagaaggcagaagcactgtgactgcagacacatcctccaacagacctac 240
 |||||
 DB 181 gccccgaacttcagaaggcagaagcactgtgactgcagacacatcctccaacagacctac 240
 QY 241 ctgcacctcagcagcctgacatctgagagacacacacgctctatctatgacatgacatc 300
 |||||
 DB 241 ctgcacctcagcagcctgacatctgagagacacacacgctctatctatgacatgacatc 300
 QY 301 tactatgaatacagcagcgtctatgcttgcagacttggggccaaaggacacagtcacagtc 360
 |||||
 DB 301 tactatgaatacagcagcgtctatgcttgcagacttggggccaaaggacacagtcacagtc 360
 QY 361 tctctcaggtgagagcggttcagagcggaaggtgctctgscgtgscgagatcggacattgag 420
 |||||
 DB 361 tctctcaggtgagagcggttcagagcggaaggtgctctgscgtgscgagatcggacattgag 420
 QY 421 ctacaccagctcctcatcttccctgctgctgtctcagcagaggaagaaggtcgtatgagctgc 480
 |||||
 DB 421 ctacaccagctcctcatcttccctgctgctgtctcagcagaggaagaaggtcgtatgagctgc 480
 QY 481 aaatccagtcagagctgtctcacaacagtagaacccgaagaagattactgtgtgtatcag 540
 |||||
 DB 481 aaatccagtcagagctgtctcacaacagtagaacccgaagaagattactgtgtgtatcag 540
 QY 541 cagaagaacagagcagctcctctaagaagtgtctatctactgggcatccactaggaatctgga 600
 |||||
 DB 541 cagaagaacagagcagctcctctaagaagtgtctatctactgggcatccactaggaatctgga 600
 QY 601 gtccctgcatcgtctcagagcagatgtgacatcgtggaacagattcactcctccacacacagat 660
 |||||
 DB 601 gtccctgcatcgtctcagagcagatgtgacatcgtggaacagattcactcctccacacacagat 660
 QY 661 gtccagagcagagcagcgtgttatctactgcaagaacatctataatctaccagagcttc 720
 |||||
 DB 661 gtccagagcagagcagcgtgttatctactgcaagaacatctataatctaccagagcttc 720
 QY 721 ggcggggggcaccagctggaatacaaa 747

DB 721 ggcggggggcaccagctggaatacaaa 747

RESULT 2

ID V72072 standard; DNA; 864 BP.

AC V72072;

DT 10-MAY-1999 (first entry)

DE Fusion protein pIC1266-55.1scFv tag/his DNA.

XX Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;

KW produg-converting enzyme; cell surface antigen; treatment; cancer;

KW inflammation; rheumatoid arthritis; antibody; produg therapy system; ss.

OS Synthetic.

PN WO9851787-A2.

PD 19-NOV-1998.

PE 05-MAY-1998; 98WO-GB01294.

PR 10-MAY-1997; 97GB-0009421.

PA (ZENPE) ZENBECA LTD.

PI Blakey DC, Emery SC;

DR WPI; 1999-059700/05.

PT New gene construct expressing conjugate of targeting agent and

PT produg-converting enzyme - useful for, e.g. targeted production of

PT cytotoxic drug in vivo, especially for treatment of cancer

PS Example 16; Page 86; 100pp; English.

XX This sequence is a used in a method for obtaining a novel gene construct

CC (A) which expresses, in cells of a mammal, a conjugate (B) of a

CC cell-targeting group (I) and a heterologous produg-converting enzyme

CC (II), and (B) is directed to leave the cell for selective localisation

CC at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a

CC target site, then administration of (II) is used for targeted release of

CC cytotoxic drug, specifically for treating cancer but also inflammation

CC such as rheumatoid arthritis. In situ generation of the targeting

CC antibody increases selectivity, reducing side effects at normal tissue.

CC The method is applicable to any antibody-directed enzyme produg therapy

CC system.

SQ Sequence 864 BP; 214 A; 234 C; 232 G; 184 T; 0 other;

Query Match 73.4%; Score 548.6; DB 20; Length 864;
 Best Local Similarity 84.3%; Pred. No. 1.2e-133;
 Matches 630; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

QY 1 caggtcaagctgcaggaagtcaggagcagaactgtgagtcaggagccctcaatttg 60
 |||||
 DB 67 caggtcaagctgcaggaagtcaggagcagaactgtgagtcaggagccctcaatttg 126
 QY 61 tctctgcagagcttctggtctcaacataaagatactatgacatgggtggaacagagg 120
 |||||
 DB 127 tctctgcagagcttctggtctcaacataaagatactatgacatgggtggaacagagg 186
 QY 121 cctgaagagagcgtgagtgatgtgatattgatactcctgaagagtggtgaacatgaat 180
 |||||
 DB 187 cctgaagagagcgtgagtgatgtgatattgatactcctgaagagtggtgaacatgaat 246
 QY 181 gccccgaacttcagaaggcagaagcactgtgactgcagacacatcctccaacagacctac 240
 |||||

Db	247	aatgagaagttcaagaanaaagccacacactgactctgtatagaacaatctctccacacaaagcctac	306
Oy	241	ctgcacactcagcagcctgacatctctgaaagacaacaacgctctactatctatctgtaatgcagtcac	300
Db	307	atgcacacacacgaacccctacacctctcgaaagactcttcggtctctacttctgcaagagagaag	366
Oy	301	tacatgatgatcgcgcggtatgactgtcttgagactacgcggggccaaaggagaccagcgtacacgtc	366
Db	367	gacctatggtttacgaag---atgcatacgacactacggtggccaaaggagaccagcgtacacgtc	423
Oy	361	tcctcaagcttggaagcgggtgttcagcgcggaagctgctctcgtgcggtgctggcagatcggacattgag	420
Db	424	tcctcaggttgccggtgtgctcggcggtggtggtggtcgggtgtggcggcgagatctgacattgag	483
Oy	421	ctcacaccagctccatctctctccctggtctgtgtcagcagaagagaaagctgcctatgagctgc	480
Db	484	ctctcacagctctccatctctccctggtctgtgtcagcagaagagaaagctgcacatgagctgc	543
Oy	481	aaatcactgactgaagttctgtttaacagtagaaccccgaaagaattacttggttgatcacg	540
Db	544	aaatcactgactgaagttctgtttaacagtagaaccccgaaagaattacttggttgatcacg	603
Oy	541	cagaaacccaaggcgagctccctcaaaagtgtgtatctcacggcgagatccatctaggaattcgcga	600
Db	604	cagaaacccaaggcgagctccctcaaaagtgtgtatctcacggcgagatccatccacaggaacatccggg	663
Oy	601	gtccctgactcgtctcacagcagcagtgatctgtggaacagattcactctcacatcagcag	660
Db	664	gtccctgactcgtctcacagcagcagtgatctgtggaacagattcactctcacatcagcag	723
Oy	661	gtcgaagctgaaagacctgacagtttatctactgcgaagcaatcttatctacacgagttc	720
Db	724	gtcgaagctgaaagacctgacagtttatctactgcgaagcaatcttatctactcgtgacgtc	783
Oy	721	ggcgggggcacccaagctggaatacaaa	747
Db	784	ggtggaggcaccagaagctcgagatcaaa	810
RESULT 3			
V72059			
ID	V72059	standard; DNA; 2019 BP.	
XX	V72059;		
AC			
XX			
DT	10-MAY-1999	(first entry)	
XX			
DE	Plasmid pNG4/55.1scFv/CPG2 R6 DNA.		
XX			
XX	Conjugate; cell targeting; cytotoxic drug; prodng-converting enzyme;		
KW	cell surface antigen; treatment; cancer; inflammation; antibody;		
KW	rheumatoid arthritis; prodng therapy system; ss.		
XX			
OS	Synthetic.		
XX			
XX	WO9851787-A2.		
PN			
XX	19-NOV-1998.		
PD			
XX	05-MAY-1998;	98WO-GB01284.	
PF			
XX	10-MAY-1997;	97GB-0009421.	
PR			
XX	(ZENNE) ZENNECA LTD.		
PA			
XX			
PI	Blakey DC, Emery SC;		
XX			
XX	WPI; 1999-059700/05.		
DR	P-PSDB; W82742.		
XX			
XX			
PT	New gene construct expressing conjugate of targeting agent and		
PT	prodng-converting enzyme - useful for, e.g. targeted production of		
PT	cytotoxic drug in vivo, especially for treatment of cancer		

[illegible]

Result	4
ID	V72064
AC	V72064 standard; DNA; 2025 BP.
XX	
XX	V72064;
XX	
XX	10-MAY-1999 (first entry)
XX	
DE	Fusion protein pMG4/55.1scFv/CPG2 R6/del EcoRI DNA.
XX	
XX	Synthetic.
XX	
XX	WO9851787-A2.
XX	
XX	19-NOV-1998.
XX	
XX	05-MAY-1998; 98MO-CB01294.
XX	
XX	10-MAY-1997; 97GB-0009421.
XX	
XX	(ZENEC) ZENEC A LTD.
XX	
XX	Blakey DC, Emery SC;
XX	
XX	WPI: 1999-059700/05.
XX	P-PSDB; W82743.
XX	
XX	New gene construct expressing conjugate of targeting agent and
XX	prodrug-converting enzyme - useful for, e.g. targeted production of
XX	cytotoxic drug in vivo, especially for treatment of cancer
XX	
XX	Example 15: Page 81; 100pp; English.
XX	
XX	This sequence is a used in a method for obtaining a novel gene construct
XX	(A) which expresses, in cells of a mammal, a conjugate (B) of a
XX	cell-targeting group (I) and a heterologous prodrug-converting enzyme
XX	(II), and (B) is directed to leave the cell for selective localisation
XX	at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a
XX	target site, then administration of (III) is used for targeted release of
XX	cytotoxic drug, specifically for treating cancer but also inflammation
XX	such as rheumatoid arthritis. In situ generation of the targeting
XX	antibody increases selectivity, reducing side effects at normal tissue.
XX	The method is applicable to any antibody-directed enzyme prodrug therapy
XX	system.
XX	
XX	Sequence 2025 BP; 440 A; 604 C; 638 G; 343 T; 0 other;
XX	
XX	Query Match 73.4%; Score 548.6; DB 20; Length 2025;
XX	Best Local Similarity 84.3%; Pred. No. 1.4e-133;
XX	Matches 630; Conservative 0; Mismatches 114; Indels 3; Gaps 1
XX	
XX	1 caggtcaagctgcagagatcaggggagagaactgtgaggtcaggggctcagtaacttg 60
XX	
XX	58 caggtcaagctgcagagatcaggggagagaactgtgaggtcaggggctcagtaacttg 117
XX	
XX	61 tctctcacaagcttcgggctcacaacttaagaactctatatgatgacgtgggtgaacagag 120
XX	
XX	118 tctctcacaagcttcgggctcacaactctcaccggctcactgtgatacaactcgggagagag 177
XX	
XX	121 cctgagaaggggctgtgagtgatattgatatcctgagaggtgtgtaaaactgaatat 180
XX	
XX	178 cctgagaaggggctgtgagtgatattgatatcctgagaggtgtgtaaaactgaatat 237
XX	
XX	181 gccccgaacttcagagggcagagccactgtgactgtcagagaacatctccacaacagctac 240
XX	
XX	238 aatgagaaggttcaagaacagggcacaactcagactgtgtgtaaaactcctccacaacagctac 297
XX	

QY	241	ctgacactcagcagccctggaactctcgaaggaacaacacgctctattactgtaagtgaagc	300
Db	298	atgcacaccacacacaccccgacacctccgaaggaactctgcggtctcattacatcgtgcgaagaagagag	357
QY	301	tactatgaaatccgcagcggtctatgctctttggaactactggtggccaaggaagaccaggtcacgcgc	360
Db	358	gcatatggtttacgcg---atgcatggaactactggtggccaaggaagaccaggtcacgcgc	414
QY	361	tctccaggttgcagggcggttccaggcggaagtggtgctctgcgtgcgttcggtatccgaattgag	420
Db	415	tctccaggttgcggttgcgtgcggtgcgtgtcgtgtcgtgtgcgtgtgcgtgtgcgtgtgcgtgtgcgt	474
QY	421	ctcaaccagcttcacatcttcctcctgtctgtctcagcaagagaagaagctgcgtacgagctgc	480
Db	475	cttccacagcttcacatcttcctcctgtctgtctcagcaagagaagaagctgcgtacgagctgc	534
QY	481	aaatccagctcgaagctctgtcttaacaagtagaaccgcgaagaagattactggtgtgtacag	540
Db	535	aaatccagctcgaagctctgtcttaacaagtagaaccgcgaagaagattactggtgtgtacag	594
QY	541	cagaacaccagtgagctctcctctaaagtctgctatctacttgcgtgcattccactagtggaattcga	600
Db	595	cagagaccagtgagctctcctctaaagtctgctatctacttgcgtgcattccactagtggaattcga	654
QY	661	gtgcagagctgcgaagacccgtgcagatttattactgcgaagcaatctataatctaccagagctc	720
Db	715	gtgcagagctgcgaagacccgtgcagatttattactgcgaagcaatctataatctactctgcagagctc	774
QY	721	ggcggtgggcccacacagctcgtgaattcaaa	747
Db	775	gggtgaggtcaccaagctcgtgaattcaaa	801
RESULT	5		
ID	X01651		
AC	X01651:		
DT	10-MAY-1999	(first entry)	
DE	Bispecific tetraivalent antibody B1rABb724-1G10H6 DNA.		
XX	B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;		
KW	CD86; T cell activation; inhibitor; graft versus host disease;		
KW	transplant rejection; allograft rejection; autoimmune disease;		
KW	allergy; therapy; human; bispecific tetraivalent antibody; B1rAb;		
XX	B1rABb724-1G10H6; ss.		
OS	Chimeric - Mus sp.		
OS	Chimeric - Homo sapiens.		
OS	Chimeric - synthetic.		
XX			
FT	Key	Location/Qualifiers	
FT	CDS	1..1726	
FT		/*tag- a	
FT		/*transl_except- (pos:780..782, aa:Ile)	
FT		/*transl_except- (pos:967..969, aa:Xaa)	
FT		/*note= "Xaa- Gln-Leu-Val-Gln-Val-Gln"	
FT	sig_peptide	1..72	
FT		/*tag- b	
FT		/*note= "peb signal sequence"	
FT	mat_peptide	73..1726	
FT		/*tag- c	
XX			
XX	W09858965-A2.		
XX			
XX	30-DEC-1998		
XX			

PT mutant, particularly for treatment of tumours
 XX
 PS Claim 5; Page 31; 54pp; French.
 XX

The present sequence encodes a single chain antibody (ScFv) designated 421. The antibody binds to an epitope present in the C-terminal region of the p53 protein that includes oligomerisation and regulatory domains, specifically between positions 320 and 393. ScFv 421 is directed against p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is introduced into cells containing a mutant p53 protein, p53-dependent transactivating activity is restored. ScFv 421 is specific for p53-mutants that have lost tumour-suppressing activity and are present in tumour cells. It is particularly used to treat hyper-proliferation associated with these mutants (e.g. cancer and re-stenosis) but may also be used in vitro for studying mechanisms of activity of p53 or its mutant and to purify or detect p53.

Sequence 729 BP; 174 A; 171 C; 207 G; 177 T; 0 other;

Query Match 61.7%; Score 460.8; DB 19; Length 729;
 Best Local Similarity 79.2%; Pred. No. 7.3e-111;
 Matches 594; Conservative 0; Mismatches 132; Indels 24; Gaps 3;

QY 1 caggtcaagctgcaaggagtcaggagcaagactgtgaggtcaggggcctcagtcatttg 60
 DB 1 caggtgacgtcagcagcagctggtgagcagcgttgagtgcaaggccctcagtcagg 60
 QY 61 tctctgacagcttcgtgcttcaacattaaagactatatactgactgggtgaacagagg 120
 DB 61 tctctgacagcttcgtgcttcaacattaaagactatatactgactgggtgaacagagg 120
 QY 121 cctgaagaggcgtgagtgatgtgattatattgactccgaagagtgtaaacattat 180
 DB 121 cctgaagaggcgtgagtgatgtgattatattgactccgaagagtgtaaacattat 180
 QY 181 gcccgcaacttcacaggagcagcactgtgactgacagacacacccctccacacagactac 240
 DB 181 gcccgcaagcttcacaggagcagcactgtgactgacagacacacccctccacacagactac 240
 QY 241 ctgacactcagcagcctgacatctgagagacacacccgtctattactgtatagcagtcac 300
 DB 241 ctgacagctcagcagcctgacatctgagagacacacccgtctattactgtatagcagtcac 300
 QY 301 tactatgaataagagcgcctgcttgagactatgaggcgcaaggcgccagcgctacccgtc 360
 DB 292 -----tttaacggggagtgcttgagactatgaggcgcaaggcgccagcgctacccgtc 342
 QY 361 tctctcaggtgagggcggttcaggcagagtggtcgtcggtgagcagatcgagacattgag 420
 DB 343 tctctcaggtgagggcggttcaggcagagtggtcgtcggtgagcagatcgagacattgag 402
 QY 421 ctcaaccagcttcacatcttcctgctgctgtcagcagagagaaggtcgctatgagctgc 480
 DB 403 atgaccaccaactccactccttctgtggttacatctgagcaacacagcctccatctcttcg 462
 QY 481 aaatccagcagcagactgctgtcaacagtagaaccggaaagaataactggtcgttgatcag 540
 DB 463 aagtcacagcagcagcctcttga---cagtgatgaaagaacacattatgagtggtgtta 519
 QY 541 cagaaacccagcagcagctctcctaaagtgcgactactatgagcaccactgagggaatctga 600
 DB 520 cagagggcagcagcagcagctctcctaaagcctcactatctggtgcttaactgagacttga 579
 QY 601 gtccctgacatcgcttcacagcagctgagatctgggacagatttcacccatcagcagact 660
 DB 580 gtccctgacagcttctcactgctgagtgatcaaggacagatttcacactgaaatacacaaga 639
 QY 661 gtgcagcagcagcagcagctgctgcttacttactgcaagcaaa---tcttaatactcagaag 717
 DB 640 gtgcagcagcagcagcagcttctgcttacttacttactgctgcaagcagacacattctccgctcacg 699
 QY 718 ttcggcggggggacccaagctggaatacaaa 747

Db 700 ttcggctgctgacccaagctggaatacaaa 729

RESULT 11

ID T86234 standard; cDNA; 749 BP.

AC T86234;

DT 24-NOV-1997 (first entry)

DE Anti-human protein p53 single chain antibody ScFv 421 cDNA fragment.

XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;

XX substitution; replacement; transactivation; viral protein VP16; HSV;

KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;

KW tumour suppression; apoptosis; single chain antibody variable domain;

SS.

XX Mammalia.

OS Synthetic.

PN WO9704092-A1.

PD 06-FEB-1997.

XX 17-JUL-1996; 96WO-FR01111.

XX 19-JUL-1995; 95FR-0008729.

XX (RHON) RHONE POULENC RORER SA.

XX Bracco L, Consallier E.

XX WPI; 1997-132633/12.

XX New p53 variants e.g. with oligomerisation domain replaced by

XX leucine zipper useful for treating hyper-proliferative disorders,

XX esp. cancer and restenosis

XX Example A; Pages 96-97; 133pp; French.

XX Claimed variants of protein p53 have at least part of the

XX oligomerisation domain deleted and replaced by a leucine zipper

XX domain. The mutants preferably also have at least part of the p53

XX transactivation domain (amino acids 1-74) deleted and replaced by

XX the transactivating domain (TD) from herpes simplex virus viral

XX protein VP16 (amino acids 411-490) or by a protein domain able to

XX bind selectively to a transactivator, especially a single-chain

XX antibody variable domain (ScFv). The present sequence represents

XX the NcoI-HotI fragment of cDNA coding for the anti-p53 single-chain

XX antibody ScFv 421. The fragment contains an ATG initiation codon

XX (precise location is not indicated) and no termination codon. The

XX p53 variants are more active and more stable tumour suppressors and

XX apoptosis-inducing agents than wild-type p53 and are active where

XX dominant negative or oncogenic mutants, nor by other cellular

CC proteins (because the leucine zipper domain prevents formation of

CC inactive mixed oligomers).

XX

XX

XX

XX

XX

XX

Sequence 749 BP; 173 A; 179 C; 221 G; 176 T; 0 other;

Query Match 61.3%; Score 457.6; DB 18; Length 749;
 Best Local Similarity 78.9%; Pred. No. 5e-110;
 Matches 592; Conservative 0; Mismatches 134; Indels 24; Gaps 3;

QY 1 caggtcaagctgcaaggagtcaggagcaagactgtgaggtcaggggcctcagtcatttg 60
 DB 10 caggtgacgtcagcagcagctggtgagcagcgttgagtgcaaggccctcagtcagg 69
 QY 61 tctctgacagcttcgtgcttcaacattaaagactatatactgactgggtgaacagagg 120

```

Db      70  |||||tcttcagcagctctcgtctcaacataaagactactatagtcagcgggtgaagcagag 129
Qy      121 cctgaagaagcgtcgtgaagtgatgatataatgatcccgagagtggtgaactgatat 180
Db      130 cctgaacaaaggccttgagtgatgataatgatacccgagaaatggtgatataat 189
Qy      181 gccccgaacttcacagggcagagcactgtgactgacagacacacccccaacacagctac 240
Db      190 gccccgaacttcacagggcagagcactgactgacagacacacccccaacacagctac 249
Qy      241 ctgacacacagcagcctgacatctgagagacacacccgtctatctgataatgacatc 300
Db      250 ctgacacacagcagcctgacatctgagagacacacccgtctatctgataat----- 300
Qy      301 tactatgaatacagcagcctgcttgagactatgggccaagggacacacgctcacgc 360
Db      301 -----tttaaggagatgcttgagactatgggccaagggacacacgctcacgc 351
Qy      361 tccctcagtgagagcgttcacagcagagtgctcgtcggtgagcagatcgacattag 420
Db      352 tccctcagtgagagcgttcacagcagagtgctcgtcggtgagcagatcgacattag 411
Qy      421 ctacccagctccatctccctgctgctgctcagcagagaggaagtcgctatgagctgc 480
Db      412 atgacccaactccactccactctgtcgttaccatgagcaacacagcctccactctgc 471
Qy      481 aatccagtcagagctgtgtcaacaaagacccgaagaatattgctgtgtatcag 540
Db      472 aagtcagtcagagcctctgga---tagtgatgaaagacacattgattggtgtta 528
Qy      541 cagaacacagcagcagctcctctaagtcagctgactgagcagcagcagcagcagcagc 600
Db      529 cagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 588
Qy      601 gtcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660
Db      589 gtcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 648
Qy      661 gtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 717
Db      649 gtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 708
Qy      718 ttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 747
Db      709 ttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 738

RESULT 12
ID      T86221 standard; cDNA; 1611 BP.
XX      T86221;
XX      24-NOV-1997 (first entry)
DE      Human p53 protein variant S-325 coding sequence from PEC176.
XX      Leucine zipper domain; LZD: oligomerisation domain; mutant; mutein;
XX      substitution; replacement; transactivation; viral protein VP16; HSV;
XX      anti-oncogene; hyperproliferation; cancer; restenosis; SCFV;
XX      tumour suppression; apoptosis; single chain antibody variable domain;
XX      ss.
XX      Chimeric - Homo sapiens.
OS      Chimeric - Herpes simplex virus.
XX      Synthetic.
XX      Key      Location/Qualifiers
XX      QDS      1..1611
XX      FT      /tag=a
XX      FT      /product=S-325
XX      FT      /note="Open reading frame ends with two tandem

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FT      termination codons"
XX      WO9704092-A1.
PN      06-FEB-1997.
XX      17-JUL-1996; 96WO-FR01111.
XX      19-JUL-1995; 95FR-0008729.
PR      (RHON ) RHONE POULENC RORER SA.
PA      Bracco L, Conseiller E.
XX      WPI: 1997-13263/12.
XX      P-PSDB: W28491.
PT      New p53 variants e.g. with oligomerisation domain replaced by
PT      leucine zipper - useful for treating hyper-proliferative disorders,
PT      esp. cancer and restenosis
PS      Claim 42; Pages 88-90; 133pp; French.
XX      CC      Claimed variants of protein p53 have at least part of the
XX      CC      oligomerisation domain deleted and replaced by a leucine zipper
XX      CC      domain. The mutants preferably also have at least part of the p53
XX      CC      transactivation domain (amino acids 1-74) deleted and replaced by
XX      CC      the transactivating domain (TAD) from herpes simplex virus viral
XX      CC      protein VP16 (amino acids 411-490) or by a protein domain able to
XX      CC      bind selectively to a transactivator, especially a single-chain
XX      CC      antibody variable domain (SCFV). The present sequence encodes
XX      CC      a specifically claimed p53 variant designated S-325 and comprising
XX      CC      a SCFV domain, amino acids 75-325 of human wild-type p53 and a
XX      CC      leucine zipper domain at the C-terminal. The p53 variants are
XX      CC      more active and more stable tumour suppressors and apoptosis-inducing
XX      CC      agents than wild-type p53 and are active where the wild-type protein
XX      CC      is not, i.e. they are not inactivated by dominant negative or oncogenic
XX      CC      mutants, nor by other cellular proteins (because the leucine zipper
XX      CC      domain prevents formation of inactive mixed oligomers).
XX      SQ      Sequence 1611 BP; 369 A; 443 C; 458 G; 341 T; 0 other.

Query Match      61.3%; Score 457.6; DB 18; Length 1611;
Best Local Similarity 78.9%; Pred. No. 6e-110;
Matches 592; Conservative 0; Mismatches 134; Indels 24; Gaps 3;

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Qy      61 tcttcacagcctctcgtctcacaactaaagactaatatgactctggttgaaacagag 120
Db      67 tcttcacagcctctcgtctcacaactaaagactaatatgactctggttgaaacagag 126
Qy      121 cctgaagaagcgtcgtgaagtgatgatataatgatcccgagagtggtgaactgatat 180
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Db      187 gccccgaacttcacagggcagagcactgtgactgacagacacacccccaacacagctac 246
Qy      241 ctgacacacagcagcctgacatctgagagacacacccgtctatctgataatgacatc 300
Db      247 ctgacacacagcagcctgacatctgagagacacacccgtctatctgataat----- 297
Qy      301 tactatgaatacagcagcctgcttgagactatgggccaagggacacacagcagctgc 360
Db      298 -----tttaaggagatgcttgagactatgggccaagggacacacagcagctgc 348
Qy      361 tccctcagtgagagcgttcacagcagagtgctcgtcggtgagcagatcgacattag 420

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 01:29:16 ; Search time 2148.34 Seconds
(without alignments)
1509.669 Million cell updates/sec

Title: US-09-297-181-3

Perfect score: 747

Sequence: 1 caggtcaagtcgagcagtc.....gcaccaagctggaatcaaa 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 12370408 seqs, 2170871038 residues

Total number of hits satisfying chosen parameters: 24740816

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_NA:*

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3: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	100.0	747	16 US-09-297-181-3	Sequence 3, Appl
2	510.2	68.3	1725	18 US-09-468-029-57	Sequence 57, Appl
3	504	67.5	759	16 US-09-235-073-10	Sequence 10, Appl
4	501.6	67.1	1668	18 US-09-468-029-59	Sequence 59, Appl
5	460.8	61.7	729	16 US-09-297-181-1	Sequence 1, Appl
6	457.6	61.3	749	13 US-08-983-035-46	Sequence 46, Appl
7	457.6	61.3	1611	13 US-08-983-035-37	Sequence 37, Appl
8	452.8	60.6	768	13 US-08-930-480-4	Sequence 4, Appl
9	445.2	59.5	714	21 US-09-559-019-30	Sequence 30, Appl
10	443.6	58.7	1679	17 US-09-364-088-15	Sequence 15, Appl
11	438.4	58.7	1679	19 US-09-523-279-15	Sequence 15, Appl
12	438.4	58.7	1679	19 US-09-523-279-15	Sequence 15, Appl
13	438.4	58.7	1679	19 US-09-523-279-15	Sequence 15, Appl
14	438.4	58.7	1679	19 US-09-523-279-15	Sequence 15, Appl
15	435.4	58.3	804	18 US-09-468-029-26	Sequence 26, Appl
16	424	56.8	924	15 US-09-171-025-3	Sequence 3, Appl
17	424	56.8	930	15 US-09-171-025-3	Sequence 3, Appl
18	407	54.5	789	18 US-09-468-029-75	Sequence 75, Appl
19	397.4	53.2	728	23 US-09-656-466-26	Sequence 26, Appl
20	394.2	52.8	1518	18 US-09-445-375A-5	Sequence 5, Appl
21	394.2	52.8	2090	18 US-09-445-375A-6	Sequence 6, Appl
22	377.2	50.5	819	55 US-09-523-095A-33	Sequence 33, Appl
23	377.2	50.5	828	55 US-09-523-095A-31	Sequence 31, Appl
24	375.4	50.3	726	9 US-08-553-497-29	Sequence 29, Appl
25	375.4	50.3	2165	3 US-07-990-263-6	Sequence 6, Appl
26	375.4	50.3	2165	3 US-07-990-263-6	Sequence 6, Appl
27	373.8	50.0	756	14 US-09-000-802-10	Sequence 10, Appl
28	372.8	49.9	783	21 US-09-589-870-36	Sequence 36, Appl
29	372	49.8	753	1 PCT-US00-19643-16	Sequence 16, Appl
30	372	49.8	771	19 US-09-526-738-1	Sequence 1, Appl
31	372	49.8	780	19 US-09-526-738-3	Sequence 3, Appl
32	372	49.5	792	1 PCT-US00-19643-9	Sequence 9, Appl
33	369.4	49.5	732	9 US-08-553-497-19	Sequence 19, Appl
34	368.4	49.1	741	55 US-09-523-095A-39	Sequence 39, Appl
35	368.4	49.0	819	55 US-09-523-095A-29	Sequence 29, Appl
36	366	48.8	828	55 US-09-523-095A-25	Sequence 25, Appl
37	364.6	48.8	732	9 US-08-553-497-21	Sequence 21, Appl
38	364.6	48.7	723	16 US-09-202-000-7	Sequence 7, Appl
39	364	48.6	723	16 US-09-202-000-9	Sequence 9, Appl
40	363.4	48.2	732	9 US-08-553-497-31	Sequence 31, Appl
41	359.8	47.9	726	9 US-08-553-497-27	Sequence 27, Appl
42	357.8	47.5	1460	7 US-07-989-846B-18	Sequence 18, Appl
43	354.8	47.5	1460	7 US-08-392-338-18	Sequence 18, Appl
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ALIGNMENTS

Qy	421	ctccccaagctccatcattcccgccgctggtcagcagcgaggaagaagctcgcatgagctgc	480
Db	1378	CTCCTAGTCTCCATCATTCCTTGCGCTGtGTCTGCGAGGAAAGAGGTCTATAGCTGT	1437
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Db	1438	AAGTCCAGTCAAAGTGTTTATATACAGTTCAAATCAGAAATAACTACTTGCCCTGGTACAA	1497
Qy	541	cagaaaccagggcagctctccctaaagtgctgcatctactggtgcacactaaggaatctgga	600
Db	1498	CAGAAACAGGCGAGTCTCTTAATAGTGCATGTACTGGGATCCACATAGGAATCAGAGT	1557
Qy	601	gtccctgcatcgcttcacagcagtgagctgtagctggaacagatlltcactctccatcagcagc	660
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RESULT 3
US-09-235-073-10
Sequence 10. Application US/09235073
GENERAL INFORMATION:
APPLICANT: Mark de Boer
TITLE OF INVENTION: Induction of T cell tolerance with
TITLE OF INVENTION: CD40/B7 antagonists
FILE REFERENCE: 99-1
CURRENT APPLICATION NUMBER: US/09/235,073
CURRENT FILING DATE: 1999-01-21
EARLIER APPLICATION NUMBER: 60/022,070
EARLIER FILING DATE: 1996-07-23
EARLIER APPLICATION NUMBER: PCT/US97/00438
EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 759
TYPE: DNA
ORGANISM: human
US-09-235-073-10

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	Best Local Similarity	80.3%	Pred. NO. 1.2e-134		
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QY	61	tccttcacagcttcctgcggtcttcacacatlaaagaactataatcagctgggttgaaacagag	120		
DB	61	tccttcgaaggtcttcggttaccatcattcaactgactataaagaatgaactgggtgaaagcagac	120		
QY	121	cctgaagagggcccttgagatgtgatatattgatacctcgagagctgggtgaaactgaatat	180		
DB	121	aatggaagaagccttcgagtgatctgaaatatctgacatcttactactatggtgtgactagtac	180		
QY	181	gccccgaacttcgaagggcaagggccactctggaatgcagaagaactcctcccaacacagctac	240		
DB	181	aatcgaagaattcaagggcgaagggccacatgactgttgagacaatcctcccgacacagctac	240		
QY	241	ctgcacactcagcagcctgcacatctbagaagacaacccgctattactgtaatgcagtcac	300		
DB	241	atgcagctcaacagcctgcacatctbagaagccttcgcagttactttctgtgcaagaatggac	300		

OY	301	tatatgaatcagcgcg-----tatgcttgcacactcggcgcaaggacacg	351
Db	301	tatggtctcgacgcgcggaggaggtctaactatgcttgcacactctggcgcaaggacacg	360
OY	352	gtcacgctctccctcaagctgtagcggtcttcagcgagagctgcctgcgctgvcgagtcg	411
Db	361	gtcacgctctctccctcaagctgtagcggtcttcagcgagagctgcctgcgctgvcgagtcg	420
OY	412	gaacttgcgcctcaccacgcttcctcattcttcctgctctgtgtcagtaggaaggagctgc	471
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OY	472	atgagctcaaatcactcagtcacagctgtctcaacagctgaagccgcgaagaattacttgct	531
Db	481	atgagctcgttaagcttcagtcacagctgtctcaacagctgaagccgcgaagaattacttgcc	540
OY	552	tgttatcagcagaacaacgagcgagctctctctaaagtgtctgatctacatcctgcacatag	591
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OY	652	atccagcaagtgcgacgctgtagaaccttgcagatttatattactgcgaacatctataatcta	711
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RESULT 4
US-09-468-029-59
: Sequence 59, Application US/09468029
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: B7-Binding molecules for treating immune
: TITLE OF INVENTION: diseases.
: NUMBER OF SEQUENCES: 80
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30 (EBO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/468, 029
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/EP98/03791
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 59:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1668 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
US-09-468-029-59

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				Gaps	0
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Db	2	AGCTACAGCAGCTTGACCTGAGCTGAGAGAACCCCTTCACGAGGAGATATCTTGA	61		
QY	68	cagctctctgcttcaacttaagaactatatactgactgggttgaaacagagcctgaag	127		

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RESULT 2
US-08-661-052-15
Sequence 15, Application US/08661052
Patent No. 5837243

GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 11..1667
US-08-661-052-15

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Query Match 58.7%; Score 438.4; DB 2; Length 1679;
Best Local Similarity 77.7%; Pred. No. 4.5e-115;
Matches 580; Conservative 0; Mismatches 136; Indels 30; Gaps 3;

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Db 903 GCACAGCTTCAGCTTCAACATTAAGACTCCTATATACCTGCTGAGCGAGGCGCTG 962
Qy 125 aagagggcctgagatgagatgagatattgatactcctgagagtgagtgagaaatgata 184
Db 963 AACAGGCGCTGAGAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1022
Qy 165 cgaacttcagagggcagagcagcagctgtagcagagacactcctcaacacagcctccgc 244
Db 1023 CGAAGTTCAGAGCGCAAGGCCACTTTTACTACAGACATCTCTCCAAACACCTTACCTGC 1082
Qy 245 accctagagcctgacatctgagacacacacagcgtctattactgtaatcagtcactact 304
Db 1083 AGCTAGCAGCCTGACATCTGAGGACACTCGCGTATATTATGATAGGGAGTCCGA 1142
Qy 305 atgaatacgaagcgtatgcttggactactgagggcgaagggacacagctcagctcctc 364
Db 1143 CTGGGCGCTACTAC-----TTTGACTACTGGGCGCAAGGACACCGGTACCGTCTCT 1196
Qy 365 caggtgagagcggttcagagcgagtgagctgctgagcggtgagcgagatcgagacattgag 424
Db 1197 CAGGTGAGAGGCGGTTCAGGCGGAGGTGCTGCGGCGGCGGAGCAAAAATGAGCTCA 1256
Qy 425 gccagctccactcttcctgctgctgctgtagcagcagagagagagtgagcgtacgaat 484
Db 1257 CCGAGTCTCCAGCAATCATGTCTGATCTCCAGGAGGAGAGAGTCAACCTGCACTG 1316
Qy 485 ccagtcagagctgcttcaacagtagaacccgaagaatattactggttgtagatcagcaga 544
Db 1317 COAGCTCAAGTGT-----AAGTTATATGACATGCTGCTTCAGAGCA 1355
Qy 545 aaccagggcagcttctcctaagtgctgactctactgagcactcactagaggaactcgtgag 604
Db 1356 AGCCAGGCACTTCTCCAAACTCTGAGATTATAGACATCCAACTGCTTCTGAGAGTCC 1415
Qy 605 ctgacagcttcaacagagtgagatctgagagacagatttcaactcctcaactcagcagtg 664
Db 1416 CTGCTGCTTCAAGTGGAGTGGATCTGGGACCTTCTACTCTCTCAATCAATCAAGCGAATG 1475

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APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Macintosh
SOFTWARE: Word 5.1 (Patentlin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..752
US-08-797-689-17

Query Match 53.5%; Score 400; DB 2; Length 756;
Best Local Similarity 73.9%; Pred. No. 2.5e-104;
Matches 559; Conservative 0; Mismatches 170; Indels 27; Gaps 3;
QY 1 caagtcagctgcagggcagggcaggaactgttgaggtcaggggagcctcaagtcattg 60
DB 12 CAGGTGAGCTCAGCGAGCTGTGACCTGAGCTGTGAGGCTGAGGCTGAGGAAATT 71
QY 61 tctgtcacactctctgtgcttcaaatcaagactacatactgacgtgtgtgaacagag 120
DB 72 TCTGTCAAAGCTTCTGTGCTTACGCTTATGATGATGATGATGATGATGATGATG 131
QY 121 cctgaagagggcctgagtgatgtatattgattcctcagagtggtggaactgaat 180
DB 132 CCTGACAGGCTTGTGATGATGACGATGATGATGATGATGATGATGATGATGAT 191
QY 181 gcccgcagactcagggcagggcagcactgtactgcagacacatcctccaacagcctac 240
DB 192 AATGAGAGTCAAGGCGCAGGCGACACTGACGCGGAGGAGATCTCCACACAGCCTAC 251
QY 241 ctgacactcagagcctcagacatctgagagacacacacgctctattactgttaagcagtc 300
DB 252 ATGACAGCTCAGCAGCTGACCTCTGTGTGGGCTGTGCGGTCTATTCTGTGCAAAAGAGAC 311

QY 301 -----tactatgaatacagcgtatctgcttgactacttggggcaggaccagcgtc 354
DB 312 AATAGTTCACAGAGGAGGCTTATGATGATGATGATGATGATGATGATGATGATG 371
QY 355 accgttcctcaggttgagggcgttcaagggaggggagggccttgccgtggcgtatggac 414
DB 372 ACCGTCTCTCAGGTGAGGCTGCTGGGCGGTGGTGGTGGTGGTGGTGGTGGTGGT 431
QY 415 attgagctcaccagctctcctcctcctgctgtctgacagagagagagagcgtatg 474
DB 432 ATTGAGTTCACAGGCTTCAATTCATGCTCAGATCAGATCAGATCAGATCAGATC 491
QY 475 agctgaatctcagtcagagctgttcaacagtagaaccggaagaattactgtgttg 534
DB 492 ACCGTGAGGCTCAGTCAAGATGTG-----GATACCTCTGTAGCCTGG 533
QY 535 taccagcagaaacacagggcagcttctcctaagtgctatctacagggcaccataggaa 554
DB 534 TATCAACAGAAACCAAGGCAATCTCTAACTACTATTACTGGGCAATCCACCGGAC 583
QY 595 tctgagctcctatctgctcacaagcagtgatctgagcagatctcaccatc 654
DB 594 ACTGAGTCCCTGATGCTTCAACAGGAGTGGATCTGGGACATTTCACTCACCATT 653
QY 655 agcagtgctcagcgtgaagacccctggcagtttacttactgaagcaatctata---atcta 711
DB 654 AGCAATGTGAGCTGAGTCAAGCTGCGAGATTAATTTCTGTCAGCAATATAGACGCTACG 713
QY 712 ccgagcttgccggggccaccagcctggaatcaa 747
DB 714 TGAGCTGCTGGTGGAGGACCAAGCTGAGATCAAA 749

RESULT 5

US-08-263-911-6
Sequence 6, Application US/08263911
Patent No. 5877291
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S
TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Duane C. Ulmer
STREET: P.O. Box 1967
CITY: Midland
STATE: MI
COUNTRY: US
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/263,911
FILING DATE: 21-JUN-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,263
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ulmer, Duane C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-41,014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2165 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

OY 553 atctggagctccgcgaatcgcgtctcaacgaagatgatctgggaagaagattccactctaca 652
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 DB 1794 ATCTGGGCTCCCTGATCTCCTTCACAGCAGTGCATCTGGGACAGATTTCTACTCTCTCCA 1855
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 OY 653 tcaagcagtgctcgaagctctgaagaccctggcagcttattactcgaagcaatctata--atc 709
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 DB 1854 TCACAGAGTGTGAAGACGTGAAGACCTGGCAGATTATATCTGTCTCAGCAGTATATAGCTATC 1911
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 OY 710 taccgagcttcgcgcgggggaccccaagctggaatcaa 746
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 DB 1914 CCTCACGCTGCGTCTGGGACCAAGCTGGCTTAA 1950
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RESULT 7
 US-08-553-497A-19
 Sequence 19, Application US/0853497A
 Patent No. 5844093
 GENERAL INFORMATION:
 APPLICANT: KETTERBOROUGH, C. A.
 APPLICANT: BENDIG, MARY M.
 APPLICANT: ANSELL, KEITH H.
 APPLICANT: GUSOW, DETLEF
 APPLICANT: ADAM, JAUDE
 APPLICANT: MITJANS, FRANCES
 APPLICANT: ROSELL, ELISABET
 APPLICANT: BLASCO, FRANCESC
 APPLICANT: PIJATS, JAUDE
 TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
 STREET: 2200 CLARENDON BLVD. SUITE 1400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: US
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,497A
 FILING DATE: 17-NOV-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/EP95/00978
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94104160.0
 FILING DATE: 17-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94118970.6
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: HAMLET-KING, DIANA
 REGISTRATION NUMBER: 33,302
 REFERENCE/DOCKET NUMBER: MERCK 1726
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 732 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: cDNA
 TOPOLOGY: linear
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:

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? ORGANISM: mouse
? STRAIN: Balb/c
? TISSUE TYPE: splenocytes
? IMMEDIATE SOURCE:
? CLONE: 10 D 2 (single-chain Fv, heavy and light)
? CLONE: chain plus linker)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..732
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? US-06-553-497A-19

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Query Match	49.5%;	Score 369.4;	DB 2;	Length 732;
Best Local Similarity	71.7%;	Pred. No. 1.1e-95;		
Matches 541;	Conservative	0;	Mismatches 181;	Indels 33; Gaps 3

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```

GENERAL INFORMATION:
APPLICANT: KETLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITTANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIJOLATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P. C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: mouse
STRAIN: Balb/c
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
CLONE: 5 F 1 (single-chain Fv, heavy, light chain,
CLONE: linker)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
US-08-553-497A-25
Query Match 49.3%; Score 368.4; DB 2; Length 726;
Best Local Similarity 71.6%; Pred. No. 2,2e-95;
Matches 537; Conservative 0; Mismatches 186; Indels 27; Gaps 3

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Db 1 CAGGTGAACCTGCAGAGACTCTGGGGCTGAGACTGTAAGCTTGGGGCTTACGTGAATTG 60

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Qy 181 gccccgaactctcaagggaagggcacctgtgactgcagacacatccctcaacagacctac 240

Db 181 AATGGAATTCCTCAAGACAGAGCCACACTGACTATTAACAAATCTCTCAGACAGCCTAC 240

Qy 241 ctgcacctcagcagccttgcatactgtgagacaacaacgcttacttactgttaatgagttatc 300

Db 241 ATGCAACTCAGCAGCGCTGACATCTGAGAGACTCTCGGCTATATCTACTG---TGCAGACGG 297

Qy 301 tactatgaatacagacgctatgctcttgtgactactctggggccaagggacaaagttcacgctc 360

Db 298 GACTATGATTCAGCAGCGGCTACTTGTACATACAGGGGCCAAGGACAAAGGCTCACCGTC 357

Qy 361 tccctaagttggaagcggtgtcacaggagagtgctcttgcgttggcggatcggagattgag 420

Db 358 TCTCTAGGTTGCGCGGTGCTCGGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 417

Qy 421 ctcaaccagcttccatctcttccctgtgcgtgtgcagcagaagaagagtcgtctatgagctgc 480

Db 418 CTCACCCAGCTCTCCAAACATCATGTCTGACATCTCCAGGGGGAAGAGTACCATGACCTGC 477

Qy 481 aaatccagtcagagtcgtgttcaacagtagaacccgaaagaattactgtgtgtgtatcag 540

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Qy 541 cagaacacagggcagctctccctaaagtgtctatctactcgtgggacatccatgaagatcga 600

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Qy 661 gtccagagctgaagacctgtgcagtttatactactgcagaacatcttataactacg--acg 717

Db 637 ATGGAGGCTGAAGATGCTGCCACTTATTATCTCCAGCAGTAGAGTAGTAGTACCCGCTCAG 696

Qy 718 ttccgagggggcaccaagcttgaatcaaa 747

Db 697 TTCGGTCTG36ACCAAGCTGGAATATAAA 726

RESULT 9

US-08-553-497A-21

Sequence 21, Application US/08553497A

Patent No. 5844093

GENERAL INFORMATION:

APPLICANT: KETLEBOROUGH, C. A.

APPLICANT: BENDIG, MARY M.

APPLICANT: ANSELL, KEITH H.

APPLICANT: GUSLOW, DETLEF

APPLICANT: ADAM, JAUME

APPLICANT: MITTANS, FRANCES

APPLICANT: ROSELL, ELISABET

APPLICANT: BLASCO, FRANCESC

APPLICANT: PUJOLAS, JAUME

TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD. SUITE 1400

CITY: ARLINGTON

```

STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ. ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 732 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Balb/c
STRAIN: Balb/c
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
CLONE: 3 D 3 (single-chain Fv, heavy and light chain)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..732
US-08-553-497A-21

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Query Match      48.8% Score 364.6; DB 2: Length 732:
Best Local Similarity 71.3% Pred. No. 2.6e-94:
Matches 538; Conservative 0; Mismatches 184; Indels 33; Gaps 3:

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Db 242 TGCACCTCAGACGCTTGACATCTGAGGACTGCGGCTATTACTG---TGCAGTGGG 298
Qy 302 actatgaatacagcagcgtactgtttggaactactgagggccaaggagcaacgtaaccgtct 361
Db 299 actatgatttaccagcagcagcgtattgactactgagggccaaggagcaacgtaaccgtct 358
Qy 362 cctcaggttgaagcgggttcaagcggaggttgctctgctcgggttgagtcgagtcggaattgagc 421
Db 359 cctcaggttgaagcgggttcaagcggaggttgctctgctcgggttgagtcgagtcggaattgagc 418
Qy 422 taaccagtcctcaatcttccctggtcgtgtcagcggaggaaggtcgtatgagctgta 481
Db 419 TCACCCAGTCTCCACAAATCATCATCTGCAATCTCCAGGGGAGAGGTTCACCATGACCTGCA 478
Qy 482 aatccagtcagtcgtcttcaacagtagaacccgaagaattacttggttgatcagc 541
Db 479 GTGACAGCTCAGTGT-----AGTTACATGTTACTGTGTACAC 517
Qy 542 agaaccagggcagtcctcctaaagtgtctactgtactggtcactccactaaggaattgag 601
Db 518 AGAAGACAGATCTCCGCCACACCTCTGATTTATGACACATCAACTCGCTTGGAG 577
Qy 602 tccctgagtcctcaacagcagtgatctgagacagattcactctccactcagcagag 661
Db 578 TCCTGTTGCTTCACTGAGTGGCACTGGCTGGACCTTACTCTCTCACAATCAGCCGA 637
Qy 662 tgcaggtgaagaccttgagctgttattactgaagcaactcctaactac----- 713
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; Sequence 27, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTERBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSLOW, DETLEF
; APPLICANT: ADAM, JAUME
; APPLICANT: MITTANS, FRANCESSE
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIJUNTS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0

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FILING DATE: 17-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94118970.6
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: HAMEL-KING, DIANA
 REGISTRATION NUMBER: 33,302
 REFERENCE/DOCKET NUMBER: MERCK 1726
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 726 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: mouse
 STRAIN: Balb/c
 TISSUE TYPE: splenocytes
 IMMEDIATE SOURCE:
 LIBRARY: 7 G 1 (single-chain Fv, heavy, light chain,
 LIBRARY: linker)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..726
 US-08-553-497A-27

Query Match 47.9%; Score 357.8; DB 2; Length 726;
 Best Local Similarity 70.8%; Pred. No. 2.2e-92;
 Matches 530; Conservative 0; Mismatches 192; Indels 27; Gaps 3;

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RESULT 11
 US-08-392-338A-18
 Sequence 18, Application US/08392338A
 Patent No. 5869620
 GENERAL INFORMATION:
 APPLICANT: Whitlow, Marc
 APPLICANT: Wood, James F.
 APPLICANT: Hardman, Karl
 APPLICANT: Bird, Robert
 APPLICANT: Filpula, David
 TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, NW
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/392,338A
 FILING DATE: 22-FEB-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/989,846
 FILING DATE: 20-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/796,936
 FILING DATE: 25-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldstein, Jorge A.
 REGISTRATION NUMBER: 29,021
 REFERENCE/DOCKET NUMBER: 0977.0030007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1460 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1449
 US-08-392-338A-18

Query Match 47.5%; Score 354.8; DB 2; Length 1460;
 Best Local Similarity 71.9%; Pred. No. 1.9e-91;


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; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1449
US-09-166-093-18

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Best Local Similarity 71.9%; Pred No. 1.9e-91;
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RESULT 13
US-09-166-093-18
; Sequence 18, Application US/09166093
; Patent No. 6027725

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; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Rolence, Michelle
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/166,093
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ. ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1460 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1449
US-09-166-093-18

Query Match      47.5%; Score 354.8; DB 3: Length 1460;
Best Local Similarity 71.9%; Pred No. 1.9e-91;
Matches 539; Conservative 0; Mismatches 142; Indels 69; Gaps 3;

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RESULT 14
US-09-172-019-18
; Sequence 18, Application US/09172019
; Patent No. 6103889
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 13:13:59 ; Search time 1856.43 Seconds
(without alignments)
2009.685 Million cell updates/sec

Title: US-09-297-181-1
Perfect score: 729
Sequence: 1 caggtgcagctgcagcagtc.....gcaccaagctggaatcaaa 729

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 118133 segs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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 25 385.2 52.8 804 81 A95255
 26 380 52.1 4354 12 ASY14583
 27 377.4 51.8 726 11 MMU20617
 28 377.4 51.8 864 81 A83227
 29 377.4 51.8 2019 81 A83211
 30 377.4 51.8 2025 81 A83217
 31 368.8 50.6 744 11 AX003780
 32 367.8 50.5 729 11 AF002242
 33 364.2 50.0 810 11 AF002527
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 35 361.8 49.6 722 12 SC0250761
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 Best Local Similarity 99.2%; Pred. No. 1.3e-212;
 Matches 723; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 1

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 DEFINITION Synthetic construct for anti-p53 scFv antibody (sefv421) containing linker sequence.

ACCESSION AJ131532
 VERSION AJ131532.1 GI:4033863

KEYWORDS antibody; immunoglobulin superfamily; scFv; variable region.
 SOURCE synthetic construct.

ORGANISM
 REFERENCE 1 (bases 1 to 729)

AUTHORS Caron de Fromental, C., Gruel, N., Venot, C., Debussche, L.,
 Conseilier, E., Drenth, C., Teillac, J. L., Tocque, B. and Bracco, L.

TITLE Restoration of transcriptional activity of p53 mutants in human
 tumour cells by intracellular expression of anti-p53 single chain
 Fv fragments

JOURNAL Oncogene 18 (2), 551-557 (1999)

MEDLINE 99124402
 REFERENCE 2 (bases 1 to 729)

AUTHORS de Fromental, C.
 TITLE Direct Submission

JOURNAL Submitted (16-DEC-1998) de Fromental C., U 380 INSERM, Institut
 Cochin de Genetique Moleculaire, 22 rue Mechain PARIS, 75014,
 FRANCE

FEATURES
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CDS

1. 729
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 Best Local Similarity 99.2%; Pred. No. 1.3e-212;
 Matches 723; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 4
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 DEFINITION Sequence 31 from Patent WO9704092.
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 VERSION A59381.1 GI:3714713
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 1611)
 AUTHORS Conseller, E. and Bracco, L.
 TITLE P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF
 JOURNAL Patent: WO 9704092-A 31 06-FEB-1997;
 COMMENT RHONE POULENC ROBER SA (FR)
 FEATUERS Other publication FR 2736915 970124.
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 1. 1608
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 EDLGVYCWGTHSPPLTFAGTKLELRAALQTRPAPAPAPAPAPAPAPSPSSSS
 VPSOKYOGSYGRLGFLHSGTAKSVTCAYSPLANMPCOLATCPVOLWVSTPPG
 TRVRAAIKQSOHMTYVRCRPHHRCSDSDGLAPQHLIRVEGMLRYEYLDNRTE
 RSHVYVPEPEVSDCTTIHNYMNCSSGMMNRPLITLTLEDSSGNLGRMSF
 EYRVCAQPRDRTEREENRKRKEPHHELPPGSTRALRNNTSSSQPKKRLDGLK
 ALKEKLALEBKLALEBKALVGER"

CDS
 369 a 443 c 458 g 341 t
 BASE COUNT
 ORIGIN

Query Match 98.28; Score 716.2; DB 81; Length 1611;
 Best Local Similarity 98.98; Pred. No. 1,4e-211;
 Matches 721; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 caagtcagctgcaagcagctggtggagagagctgtggtgctcagggcctcagtcgaattg 60
 Db 7 CAGGTGAGCTGCAAGAGTAAAGGGCGAGAGCTGTGGGGTCAAGGGCCTCAGTCAAGTTG 66.
 QY 61 tctctgcaagcttctggtctcaacatataaagactatataatgcaactggtggaagcagag 120
 Db 67 TCTGTGACAGCTCTGTGCTTCAACATTAAGAGACTACTATATGCACTGGTGGGAAGCAGG 126
 QY 121 cctgaacaggcctgtgagctggtgattgattgattgattcctgaagaattgataactgaat 180

Db 127 CCTGACAGGCGCTCGAGTGGATTGGATGGATTGATTCAGATAGTGCTACTGAATAT 186
 QY 181 gccccgaagttcccaaggcaaggccactatgactgtagacacatctccatatacagcctac 240
 Db 187 GCCCGGAAGTTCAGAGGCAAGGCCACTATGACTGACAGACATCTCTCAATFACAGCCTAC 245
 QY 241 ctgcaagctcaagcctgtgcatctgagacactgacgtctataatgttaatttttaaggg 300
 Db 247 CTGAGCTCAGCAGCCCTGGCATCTGAGACACACGCCCTCATATTATTTTATTTTACGGG 305
 QY 301 gatgcttgagctatttgaggccaaggagacaggttaccgctccctcaagttgagagcgt 360
 Db 307 GATGCTTGAGCTACTGAGGCGCAAGGACACAGGTACCGCTCTCTCTGAGTGAGCGCGT 366
 QY 367 TCAGGCGGAGTGGCTGTGGCGGTGGCGGATCGGATGTTTGAATGACCAACTCCACTC 426
 Db 421 actttgtcgtttaccattggaacaacagcctcactctcttgcgaagtcaagcagctc 480
 QY 427 ACTTGTGCGGTACCAATTGGACACACAGCCTCCATCTCTTGAAGTCAAGTCAAGAGCTC 486
 Db 481 ttgatagtgatgaaagacataattgaaattgtgtttacagaggccagggcaggtctcca 540
 QY 487 TTGATAGTATGGAAGACATATTGATTGTGTGTACAGAGCCAGGCACTCTCCA 546
 Db 541 aagcgctaatctatctggtgtcctaaactggaactctggaagctccctgacaggttcaagc 600
 QY 547 AAGCGCTATATCTATCTGCTGTCTAACTGAGACTCTGAGCTCTGACAGGTTACTGCG 606
 Db 601 agtggatcaggagacagattctacacgtgaaatacaacagagtgagagctgagattggga 660
 QY 607 AGTGGATCAGGAGACAGATTTCACACTGAAATCAACAGAGTGAGGCTGAGATTGGGA 666
 Db 661 gttattatgtctgctgcaaggtacacattctccgtcactgctggtgtgtgagaccactg 720
 QY 667 GTTATTATTGCTGGCAGAGTACACATTCTCCGCTCAGCTTGGTGTGGGACCAAGCTG 726
 QY 721 gaaatcaaa 729
 Db 727 GAGCTGAAA 735

RESULT 5
 AB030249
 LOCUS AB030249 912 bp DNA SYN 22-OCT-1999
 DEFINITION Synthetic Mus musculus gene for 3c10 single chain antibody,
 complete cds.
 ACCESSION AB030249.1 GI:5596361
 VERSION AB030249.1
 KEYWORDS light chain variable domain; heavy chain variable domain; 3c10
 single chain antibody.
 SOURCE synthetic construct
 ORGANISM Mus musculus
 REFERENCE 1 (sites)
 AUTHORS Okamoto, S., Yoshikawa, K., Obara, Y., Shibuya, M., Aoki, S., Yoshida, J.
 and Takahashi, T.
 TITLE Monoclonal antibody against the fusion junction of a
 deletion-mutant epidermal growth factor receptor
 Br. J. Cancer 73 (11), 1366-1372 (1996)
 MEDLINE 96249052
 REFERENCE 2 (sites)
 AUTHORS Nakayashiki, N., Yoshikawa, K., Nakamura, K., Hanai, N., Okamoto, S.,
 Mizuno, M., Wakabayashi, T., Sago, S., Yoshida, J. and Takahashi, T.
 TITLE Production of a single chain variable fragment antibody recognizing
 type III mutant epidermal growth factor receptor
 Unpublished (1999)
 REFERENCE 3 (bases 1 to 912)
 AUTHORS Yoshikawa, K. and Nakayashiki, N.
 TITLE Direct Submission
 JOURNAL Submitted (21-JUL-1999) to the DDBJ/EMBL/GenBank databases.
 Kazuhiro Yoshikawa, Aichi Medical University, Department of


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misc_feature      751..774
                  /note="encodes CDR 3"
misc_feature      811..864
                  /note="encodes C-myc peptide"
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Query Match      75.6%; Score 550.8; DB 12; Length 864;
Best Local Similarity 85.3%; Pred. No. 3.7e-160;
Matches 631; Conservative 0; Mismatches 97; Indels 12; Gaps 1;
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DB 68 AGGTTACGTCGACAGACTGCGGACAGACTTGAGAGTCAGGGGCTCAGTCAGTTGT 127
QY 62 cctgcacagcttctgcttcaacatcaataactactatgacactgggtgaagcagagc 121
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DB 128 CCGGACAGCTTCTGCTTACACATTAAACCTTAAACACTGGGTGAACAGAGGC 187
QY 122 ctgaacagggccctgagatgagatgagatgagatgagatgagatgagatgagatg 181
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DB 188 CTGAACAGGGCTCGAGTGGATTGATGATGATGATGATGATGATGATGATGATG 247
QY 182 ccccgagcttcacagagcagagccactatgactgaagacacatccctcaatacagctacc 241
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DB 248 CCCCAAGTTCCAGGACAAAGCCACTATGACTACAGACACATCTCCACACAGCCTACC 307
QY 242 tgaagctcagcagcctgggactctgagagacacgctcctatttgaattt----- 294
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DB 308 TGCAGCTCAGCGGCTGACATCTGGGGACACTCCCGCTATTCTGTAATGCTCTAATTC 367
QY 295 -----tacggggagtgcttggatgactatgaggccaagagacagctgacgctcctcag 349
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DB 368 TACGCTTCTCTCTGCTGATGAGACTACTGGGGCCAAAGGACACAGGCTCTCTCAG 427
QY 350 gtgagagcggttcaagcgagagctgctgctgctgctgctgctgctgctgctgctgctc 409
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DB 428 GTGAGAGCGGCTTACAGGGAGGAGTGGCTCTGCGGATGGCGGATGGATGTTGATGCC 487
QY 410 aaactcactcactcttggctggttaccacttgaacacacagcctcactctctcgaagtcaa 469
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DB 488 AACTCTCAGCTCTCCCTGCTATAGTCTTGAATCAAGGCTCCATCTCTTGAATCTA 547
QY 470 gtacagagcctctgagatgagatgagatgagatgagatgagatgagatgagatgagatg 529
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DB 548 GTGAGAGCATTTGACATAGTAAGAAACACCTATCTAGAAATGTTACTCAGACAGACAG 607
QY 530 gccagctctccaaagcgctactatctatctggtgtcctaactggaactctgagctccctgaca 589
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DB 608 GCCAGTCTCCAAAGCTCCTGCTCTTCAAGTTTCCAAACGATTTTCTGGGGTCCCAAGATA 667
QY 590 ggttcactcagctgagatgagatgagatgagatgagatgagatgagatgagatgagatg 649
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DB 668 GGTTCAGTGGCATGATCAGGAGACAGATTTCACACTCAAGATCACCAGAGAGTGGAGGCTG 727
QY 650 aggatctggagatgagatgagatgagatgagatgagatgagatgagatgagatgagatg 709
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QY 710 gcaccaagctggaatcaaa 729
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DB 788 GACCAAGCTGGAATCAAA 807

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VERSION          229480.1 GI:1694842
KEYWORDS         anti-abcisic acid antibody; fusion gene; immunoglobulin heavy
SOURCE           chain; immunoglobulin kappa chain; immunoglobulin variable region.
ORGANISM         house mouse.
SOURCE           Mus musculus.
ORGANISM         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                  Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE        1 (bases 1 to 747)
AUTHORS          Artaenko, O., Weller, E.W., Muentz, K. and Conrad, U.
TITLE            Construction and functional characterization of a single chain Fv
                  antibody binding to the plant hormone abscisic acid
JOURNAL          J. Plant Physiol. 144, 427-429 (1994)
REFERENCE        2 (bases 1 to 747)
AUTHORS          Artaenko, O.
TITLE            Direct Submision
JOURNAL          Submitted (10-JAN-1994) Artaenko O., Institute of Plant Genetics
                  and Crop Plant Research, Molecular Cell Biology, Corrensstrasse 3,
                  D-06466 Gatersleben, Germany
REMARK           Revised by author 26-NOV-96
                  3 (bases 1 to 747)
                  Artaenko, O., Pelsker, M., zur Nieden, U., Fiedler, U., Weller, E.W.,
                  Muntz, K. and Conrad, U.
TITLE            Expression of a single-chain Fv antibody against abscisic acid
                  creates a wilty phenotype in transgenic tobacco
JOURNAL          Plant. J. 8 (5), 745-750 (1995)
COMMENT          On Nov 28, 1996 this sequence version replaced gi:902353.
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                  /note="binding abscisic acid"
                  /product="single chain Fv antibody"
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                  YTSLSYWGQGVTVVYSSWGGSGGSGGSDIELTOSPPSVVIVPEESVTSICRSS
                  KSLTSDSDSYLFNFIQRPQSPOLLITRMSNLASGVDPDRSGSGSTFLIRSRVE
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                  /organism="synthetic construct"
BASE COUNT       163 a      183 c      218 g      183 t
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Query Match      68.6%; Score 500.4; DB 11; Length 747;
Best Local Similarity 81.0%; Pred. No. 1.8e-144;
Matches 598; Conservative 0; Mismatches 131; Indels 9; Gaps 1;
QY 1 caagtgcagctcagcagctcctgagcagagctgagtcagagggccctcagtcagtgt 60
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DB 1 CAGGTCACTGACAGAGCTTGAGCTGAGCTTGTAAGGCCAGAGGCTCAGTCAAGTTG 60
QY 61 tccctgcacagcttctgcttcaacatcaataactactatgacactgggtgaagcagagc 120
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DB 61 TCGTGCACAGCTTCTGCGTTTAAATTTAAAGACGACTATATTCATGCGGTGAAGCAGAG 120
QY 121 cctgaacagggccctgagatgagatgagatgagatgagatgagatgagatgagatgagatg 180
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DB 121 CCGAAGAGGCGCTGAGTGGATGGCAGAGATTGCTCCGACAGTGAATGTTAAATAT 180
QY 181 gccccgaagcttcagagcagagccactatgactgagagacacatccctcaatacagctacc 240
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DB 181 GTCCCGAGGTTCCAGACAAAGCCAGATTACTGACAGACATCTCTCCACACAGCCTAC 240

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Oy	241	ctcgagctcaagaagcctctgcatctagaagacctgcgcctatattgt-----aat	291
Dd	241	ctgcgtgcttcagagcctacatctatgagacatgccgtattactgtcttgaagagat	300
Oy	292	tttaacggagatgctttgactattgaggccaaggacaacgagtcacgctctcctaagt	351
Dd	301	actttgtacacactcgcctgctgtattggggccaaaggaccacacgcgtcaccccttcctatagg	360
Oy	352	ggaagcgagttcagggcgggaagtggcctctgcgcgttgagcgatgagttttgatgaccaa	411
Dd	361	ggagcgggttcagggccgagagtgctcttgccgctggcggatccgacattgaactcacccag	420
Oy	412	actccactactcttgcggttaacattggaacaacacgcctccatctcttgcgaattcaat	471
Dd	421	tctccacacctctgtgattgtcatcttcctggagagtcagttccatctccgcaggtcaagt	480
Oy	472	cggagcctcttgatgatatggaagaagacattggaattggtttgtaagaaggccaagc	531
Dd	481	aaagattctcttattatgtaatggcgcacttttacttatttttggttcttcgacgaagccagac	540
Oy	532	cagctctccaaagcgacctaatctactgtygtctaaactgtaactctgagttccctgcagag	591
Dd	541	caggtctccacactcctctgattatgcgattgcgaaccttgctctcagagattccacagag	600
Oy	592	ttcacttgcagtgatcagaagacagattccaactggaataataacagaaatgtaggttgag	651
Dd	601	ttcacgtggcagtgggcgcagaaactgattccacactgaatgacgtaagatggcggcttgag	660
Oy	652	gattttgggaagttaatatctgcctgcgaaggtacacattctccgctcaagttcgtgtctgc	711
Dd	661	gattatggggtttattactgtaatgcgaacatcgagagattaccgcgtcagttcgggtctggg	720
Oy	712	accaagcttgcgaatacaaa	729
Dd	721	accaagctgcgacctgaaa	738

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RESULT      8
LOCUS       XXU44796
DEFINITION  XXU44796      732 bp      mRNA
SYN         SYN         03-FEB-1996
DEFINITION  Synthetic construct single-chain anti-acetylaminofluorene antibody
            mRNA, from PCR amplified mouse VH and VL regions, partial cds.
ACCESSION   U44796
VERSION     U44796.1  GI:1177222
KEYWORDS
SOURCE      synthetic construct.
            synthetic construct
            artificial sequence.
REFERENCE   1 (bases 1 to 732)
AUTHORS     Guesdon,J.-L. and Muller,B.H.
TITLE       Direct Submision
            Submitted (05-JAN-1996) Jean-Luc Guesdon, Institut Pasteur, 28, rue
FEATURES
            du Docteur Roux, Paris, 75015, France
SOURCE      Location/Qualifiers
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Best Local Similarity	78.3%;	Pred. No. 5.9e-137;		
Matches 571;	Conservative 0;	Mismatches 158;	Indels 0;	Gaps 0

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QY	61	tccctgcacagcttcctggtcttcaacattaaagactactatatagtcactggtgtgaagcagag	120
Db	61	TCCGTCAAGGGTTCTTGCGCTACACTTACTACTGATGATGCATGGGTAAACAGAG	120
QY	121	ccctgaacagggcctcgtgaggttgatttgtagtattgatactctgaagaatgtgtactgaatat	180
Db	121	CCTGCAAGGGTCTCGAATAGGATTTGGATATGATTCCTGTACTGTGTTTACTAATTAC	180
QY	181	gcccgcgaattccagggcagaagccacactatgcctgcagacacatccctccaataagcctac	240
Db	181	AATAGAGATTCAAGGACCAAGGCCACACTTACTCTGACAGCAAAATCTCTCAGCACGCTTAC	240
QY	241	ctgcagactcagcagcgcctgagcatctgaggaacactgcgcgtctattattgtaattttacagg	300
Db	241	ATGCAACTGAGACACCTTGACATCTGAAGACTCTGCAAGTCTATTACGTGCAAGAGGGA	300
QY	301	gatyctttgtagctatttggtggccaaagggaccagagtcacgctctccctcaagttgagggcgt	360
Db	301	CTATACGGAAACTCTGCGGGCCAAAGGGACACGCGTCAACGCTTCCTCAATGTGAGGCGGT	360
QY	361	tcagcagcgaagtgtgctctgcgcgtgtggcgatcggaigtgtttgtagcccaactcaactc	420
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QY	421	actttgcgtgttaccatttggacaacacagcctccatctcttgcagaatcaagtcagagcctc	480
Db	421	TCCCTGGCTGTCACTCTTTGGAGATCAACGCTCCATCTCTGCAAGTCTAATCAGAGCCTT	480
QY	481	ttgatatgtgttggaaagacatatgtgaattgtgtgttacagagggccagggccagcttcca	540
Db	481	GAAAACAGTATGGAAACACACTTATTTGAATGTGACTCCACGAACACAGGCCAGTCTCCA	540
QY	541	aagcgctaactctctcgtgggtcctaaactgtagtactctgtagtccctcgacaggttcatctgc	600
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QY	601	agttgatacagagacaagattccacactgtaaaatcaacacagagttgtaggctctgagatttggga	660
Db	601	AGTGATCAAGSGAAGATTTTCACACTGAATAATCAGCAAGATGTGAAGCTAGAGATTGGGA	660
QY	661	gtttattattctgtgcagaaglaacacattctcgctcgcacgttcagttcgtgtgcaccaaagctg	720
Db	661	GTTATTATTCTTCCTCCCAACTTACACATGTCCCGTACACGTTTCGAGGGGGGACCAAGCTG	720
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Db	721	GAGCTGAAA 729	

RESULT	9			
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LOCUS	AC013153	747 bp	mRNA	SVN
DEFINITION	Synthetic construct for anti-p53 ScFv antibody (scFv1ID3) containing linker sequence.			

ACCESSION AJ131533
 VERSION AJ131533.1 GI:4033867
 KEYWORDS antibody; immunoglobulin superfamily; scFv; variable region.
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 747)
 Caron de Fromental, C., Gruel, N., Venot, C., Debussche, L.,
 Conseiller, E., Dureau, C., Teillaud, J. L., Tocque, B. and Bracco, L.
 Restoration of transcriptional activity of p53 mutants in human
 tumour cells by intracellular expression of anti-p53 single chain
 Fv fragments
 JOURNAL Oncogene 18 (2), 551-557 (1999)
 MEDLINE 99124402
 REFERENCE 2 (bases 1 to 747)
 de Fromental, C.
 TITLE Direct Submission
 JOURNAL Submitted (16-DEC-1998) de Fromental C., U 380 INSERM, Institut
 Cochin de Genetique Molculaire, 22 rue Mechain PARIS, 75014,
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 /db_xref="GI:4033868"
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 Query Match 63.2%; Score 460.8; DB 12; Length 747;
 Best Local Similarity 79.2%; Pred. No. 3.6e-132;
 Matches 594; Conservative 0; Mismatches 132; Indels 24; Gaps 3;

QY 181 gccccgaagttccagagcgaagccactatgactgacagacacacccrcaatcagcttac 240
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 Db 181 GCCCGAAGTCCAGGCGCAGGCGCACTGTGACTGCGACACATCTCCACACAGCCTAC 240
 QY 241 ctgcagctcagcagcctggcatctggagacacacgcctctatatgtat----- 291
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 Db 241 CTGCACCTCAGCAGCCTGACATCTGAGACACACACCGTCTATTACTGTATGACATC 300
 QY 292 -----tttacgggagtgcttggactattgggccaaggaagcagctacagtc 342
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 Db 301 TACTAGATACGACGCGATGCTTGGACTACTGGGCGCAAGGACACGCGACCGTC 360
 QY 343 tctcagtggtggagcgttcagcagcaggtgtgtcgtggggtggcagatgtttg 402
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 Db 361 TCCTCAGGTGGAGCGGTCAGCGGAGGCTGTGGCGGTGGCGATCGACATTGAG 420
 QY 403 atgacccaactcactcactctgtgtgttaccattggacaacacagccctcactctgc 462
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 Db 421 CTCACCCAGTCTCAGCTTCCCTGCTGTGTGACGAGAGAGAGTCCGTATGACCTGC 480
 QY 463 aagtcagtcagagcctcttga--tagtatygaagacacatattgaattgtgtta 519
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 Db 481 AATCCAGCAGAGTCTGTTCACACAGTACAGACCCGAAGATTAATCTTGCTGTATCAG 540
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 Db 541 CAGAAACAGGCGAGCTCTCTTAAGTCTGATCTAGTGCGCATCCCTAGGGATTTGGA 600
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 Db 601 GTCCCTGATCGCTTCACAGGCACTGATGTGGACAGATTCTACACACACACAGT 660
 QY 640 gtgagagctgagagatttggagttatattatctggtgcaaggtacacattccgcctcag 699
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 Db 661 GTCGACGCTGAGACCTGCGACATTTATCTCGAAGCAA---TCTTATATACACGACG 717
 QY 700 ttctgtctgagcagcagctggaatcaaa 729
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 Db 718 TTCGCGCGGGCGACCAAGCTGGAATCAAA 747
 RESULT 10
 AF064776 738 bp mRNA SYN 21-MAY-1998
 LOCUS AF064776
 DEFINITION Synthetic Mus musculus anti HIV-1 p17 scFv mRNA, complete cds.
 ACCESSION AF064776
 VERSION AF064776.1 GI:3142707
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct.
 synthetic construct.
 artificial sequence.
 REFERENCE 1 (bases 1 to 738)
 AUTHORS Tewari, D., Goldstein, S., Norkins, A.L. and Zhou, P.
 TITLE Single chain antibody to HIV-1 p17
 JOURNAL J. Immunol. (1998) in press
 REFERENCE 2 (bases 1 to 738)
 AUTHORS Tewari, D., Zhou, P. and Norkins, A.L.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAY-1998) National Institute of Dental Research,
 National Institutes of Health, 9000 Rockville Pike, Bethesda, MD
 20892, USA
 FEATURES
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DEFINITION	Sequence 4 from Patent W09749726.					
ACCESSION	A68604					
VERSION	A68604.1	GI:4759633				

KEYWORDS
SOURCE

SOURCE
ORGANISM

REFERENCE

AUTHORS

TITEL

JOURNAL

COMMENT

FEATURES

COPIES

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DEFINITION Mus musculus synthetic construct for anti-guinea pig C5 ScFv
ACCESSION AJ250763
VERSION AJ250763.1 GI:6272278
KEYWORDS antibody; heavy chain; immunoglobulin superfamily; light chain;
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 759)
REFERENCE
AUTHORS Link,C., Hawlisch,H., Meyer zu Vilsendorf,A., Gylernuez,S., Nagel,E.
and Koehl,J.
TITLE Selection of phage-displayed anti-guinea pig C5 or C5a antibodies
and their application in xenotransplantation
JOURNAL Mol. Immunol. 38, 1235-1247 (1999)
REFERENCE
AUTHORS Link,C., Hawlisch,H., Meyer zu Vilsendorf,A., Gylernuez,S., Nagel,E.
and Koehl,J.
TITLE Selection of phage-displayed anti-guinea pig C5 or C5a antibodies
and their application in xenotransplantation
JOURNAL Mol. Immunol. 38, 1235-1247 (1999)
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Db		677	AGGACTCTGGGGATTATTCTGCTCTCAAGATACACATGTTCCGTGGACGTTCCGTGGAG	736
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ACCESSION	AX003776			
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REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases: 1 to 753)			
TITLE	Kufner P. and Raum T.			
JOURNAL	Method of identifying binding site domains that retain the capacity			
FEATURES	Patent: WO 9925818-A 27-MAY-1999.			
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GenCore version 4.5
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Listing first 45 summaries

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4	232.8	31.9	614	90	AM405187	AM405187 UI-HF-BL0
5	229	31.4	454	90	AM406883	AM406883 UI-HF-BL0
6	227.2	31.2	444	90	AM406448	AM406448 UI-HF-BL0
7	223.4	30.6	363	7	AA464313	AA464313 zx78c12.r
8	223.4	30.6	425	24	AT734035	AT734035 z56602.r
9	223.4	30.6	442	7	AA405415	AA405415 z56602.r
10	221.8	30.4	488	90	AM405725	AM405725 UI-HF-BL0
11	219.2	30.1	468	136	BE829853	BE829853 RC6-ET007
12	218.2	29.9	456	90	AM404683	AM404683 UI-HF-BL0
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14	214.8	29.5	911	106	BE286958	BE286958 601092470
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35	192	26.3	486	95	AM806391	AM806391 MR4-UM011
36	191.2	26.2	459	95	AM806364	AM806364 MR4-UM011
37	191	26.2	374	9	AA602059	AA602059 n095b02.s
38	190.8	26.2	596	106	BE310080	BE310080 601091549
39	190.6	26.1	601	172	AZ447391	AZ447391 1M0244H01
40	189.8	26.0	554	174	AZ505978	AZ505978 1M0346J22
41	189.6	26.0	534	93	AM658126	AM658126 93905.MAR
42	188.2	25.8	456	104	BE144269	BE144269 MR0-HT016
43	187.2	25.7	544	93	AM655441	AM655441 106209.MA
44	186.8	25.6	287	8	AA496610	AA496610 zv38g06.r
45	184	25.2	439	104	BE136816	BE136816 ug56b01.Y

ALIGNMENTS

RESULT 1
 BE306420 * 1057 bp mRNA
 LOCUS 601103347p1 NC1 CGAP_Lu29 Mus musculus cDNA clone IMAGE:3495755 5',
 DEFINITION
 mRNA sequence.
 BE306420
 ACCESSION BE306420.1 GI:9159604
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.


```

IMAGE:3057394.5', mRNA sequence.
ACCESSION AM405772
VERSION AM405772.1 GI:6924829
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 471)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.L.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/db/seq/image/image.html
Seq primer: M13 Forward.

FEATURES
SOURCE
location/Qualifiers
1..471
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3057394"
/clone_1db="NIH-MGC.37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LIT)"
/notes="Vector: pUT73-Pac; Site.1: NotI; Site.2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 107 a 124 c 119 g 121 t
ORIGIN

Query Match 31.9%; Score 232.8; DB 90; Length 471;
Best Local Similarity 79.3%; Pred. No. 2.1e-59;
Matches 276; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

382 ggtggcgcgtgcgtatggtttgtagtgcacaaatccactcacttcttggtggtaccattgga 441
Db 15 GGATCCAGGCGAGATATTGTGATGACCCAGCATCCACTCTCTCTCCGTCACCCCTGGA 74

442 caaccagccctcatctctctgcaagtcacagtcagcctcttgtagatgtagtgaagaca 501
Db 75 CAGTGGCGCTCATCTCCGCAAGCTCATGTACTGACAGCTCTCTGATATGATTAAGAC 134

502 taattgaattggttcttacaagagccagagccagtccttccaaagcgctaatctatctg 561
Db 135 TATTGTGATTGTGACTGCGAAGACGACGCGCAGTCTCCACAGCTCTGATATGAGTT 194

562 tctaaatcggaattcggagatcccttcaacagtggttccattcgatcgatcaggacagattc 621
Db 195 TCCAAACCGGTTCTCGGAGTGCACAATAGGTTCACTGTGCGAGGGGTCAAGGACACATTTC 254

622 aacatgaaatcaacagagtaggagctgaggaattgggagatttatatgctggcgaagt 681
Db 255 ACACGGAATAATACCCGGGTGAGGCTGAGGATGTTGGGTTTATTACTGCAATCGAAAGT 314

682 acacattctccgctcagcttcggttcgtagccacgaagctggaatcaaa 729
Db 315 ATACAGCTTCCTCTCCTCACTTTCCGCGGAGGAGGACCAAGTGGAGATCAAA 362

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	AM405187	614 bp	mRNA	EST	16-FEB-2000
DEFINITION	UT-HF-BL0-acb-c-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058546 5', mRNA sequence.				
ACCESSION	AM405187				
VERSION	AM405187.1 GI:6924244				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 614) NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/. National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999).				
COMMENT	Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E Consortium/LNLN at: www.bio.lnl.gov/dbrr/image/image.html Seq primer: M13 forward.				
FEATURES	Location/Qualifiers				
source	1..614 "/organism='Homo sapiens' '/db_xref='taxon:9606' '/clone_image=3058546" '/clone_lib="NIH_MGC_37" '/tissue_type="lymph" '/cell_type="germinal center B cells" '/cell_line="MCG85" '/lab_host="DHIOB (LTR)" '/note="Vector: p1773-Pac; Site.1: NotI; Site.2: Eco RI." Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louisa M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldi, Ph.D. and M. Bento Soares, Ph.D."				
BASE COUNT:	146 a 169 c 160 g 139 t				
ORIGIN					
Query Match	31.9%; Score 232.8; DB 90; Length 614;				
Best Local Similarity	79.3%; Pred. No.2,3e-59;				
Matches 276; Conservative	0; Mismatches 72; Indels 0; Gaps 0;				
Dy	382 gtgtgagatcggaattttgatggccaactcaactcttcgcgttacattga 441				
Dd	55 GGATCAGGCAAGAATTGTGATGGACCAGACTCACCTCTCTGTGCCGTCCACTTGGA 114				
OY	442 caaccaggcccatcttcttgacaagtcaagtcagaaccttttgtatagtagtaaaagaaa 501				
Dd	115 CAGCGGCGTCCTCATCTCTGCAAGCTGTAGTGCAGCCCTCTGCAATAGTAGTAAGAAAGAC 174				
OY	502 tatattaattgtgtgttcacagagcccaagcccagttcccaaagcgctaacttatctgtgtg 561				
Dd	-175 TATTGTATTGTGTACTGCAAGAACCCAGGCCAAGTCTCCACACACTCTTATATATAAGTT 234				
OY	562 cttaaagtgaactctgtagtcccttacagaggtcaccttgagtcagtagatacaggaagatatlc 621				
Dd	235 TCACAACGGTTCCTGTGGAGTGCACATAGGTTCACTGGAGCGGGTCAAGGACAGATTTC 294				
OY	622 acactgaaatcaacagagtggaagctgtagaatlttgysagttatlatgtctgcagaagt 681				
Dd	295 ACACAGGCAACCAACCTGCTGGAGGCTGACGATGTGTGGGTTTTATTACGCATCCAAGT 354				
OY	682 aaacattctgcgtcagcttgcgtgtgtcggaccaagtcgtgnaataaaaa 729				
Dd	355 ATACAGCTTCTCGACAGTTGGCCCAAAGGACCAAGTGTGAATATAA 402				

RESULT	5
LOCUS	AM406883 454 bp mRNA EST 16-FEB-2000
DEFINITION	UI-HF-BL0-aqf-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061493 5', mRNA sequence.
ACCESSION	AM406883
VERSION	AM406883.1 GI:5925940
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eunaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 454)
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www.bio.lnl.ni.gov/bdrip/image/image.html Seq primer: M13 Forward. Location/Qualifiers 1..454 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3061493" /clone_lib="NIH_MGC_37" /tissue_type="lymph" /cell_type="germinal center B cells" /lab_host="DH10B (LT1)" /note="Vector: p17r3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT	104 a 122 c 114 g 114 t
ORIGIN	
Query Match	31.4%; Score 229; DB 90; Length 454;
Best Local Similarity	78.5%; Pred. No. 2.9e-58;
Matches 274; Conservative	0; Mismatches 75; Indels 0; Gaps 0;
OY	381 cggtagcgatcgattgtttgatgaccacaactccactcaattgttcggttacattgg 440
DB	3 CGAGGCCAATGGGGAATTATGTGATGACTCAGCTCCACCTCGCCCGTCACCCCTGG 62
OY	441 acaacagctccatctcttgccaagtcaaggacctcttggaatgtagaaagaac 500
DB	63 AGAGCGGGCTCACTCCTCGAGGCTTAGTGACAGGCTTCGCAATGATGATAC 122
OY	501 ataattgaattggttgttaccagaagccagagcagctccaagcgccatatcatctgt 560
DB	123 CAAATTGGATTGTTGTAACCTGCACAGAAGCCAGGCAAGTCTCCACAGCTCATTTGGG 182
OY	561 gtctaactgcgactctgagctccctgcacaggttcaactgagcagtagtaagaacagatt 620
DB	183 TTCTATATCGGGCTCCGGGGTCCCTGCACAGGTTTCAGTGGCACTGATCAGGACGATT 242
OY	621 cacactgaataaccaaagagtgagagctgagatttgtagagatttatgtgtgcaagg 680
DB	243 TCACTGAATAATCACAAAGTGAGGCTAGAGATGTGGGGATTATTAATCATGATCAAC 302

OY		681	taccatcttcgcgtccacgcttgcgttgctggcagcaacttgttaaatcaa	729
Dd	303	TCTACAACTCCTCAAGACGTTGGCCCAAAGSACAAGGTGAATTCATA	351	
RESULT		6		
LOCUS		AM406448	444 bp	mRNA EST 16-FEB-2000
DEFINITION		UI-HF-BLD-acr-c;-05'-0'-UI-T1 NIH-MGC_37 Homo sapiens CDNA clone IMAGE:3060080 5' mRNA sequence.		
ACCESSION		AM406448:		
VERSION		AM406448.1	GI:6925505	
KEYWORDS		EST.		
SOURCE		human.		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS		1 (bases 1 to 444)		
TITLE		NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.		
JOURNAL		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT		Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www.bio.llnl.gov/dbrr/image/image.html Seq primer: M13 Forward. Location/Qualifiers 1..444 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image=3060080" /clone_lib="NIH_MGC_37" /tissue_type="lymph" /cell_type="germinal center B cells" /cell_line="MGC85" /lab_host="DHOB (LTL)" /note=Vector: pTZ19-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT		103 a	122 c	114 g 105 t
ORIGIN				
Query Match	:	31.2%	Score 227.2;	DB 90; Length 444;
Best Local Similarity	:	79.8%;	Pred. No. le-57;	Mismatches 68; Indels 0; Gaps 0;
Matches	268;	Conservative	0;	Mismatches 68; Indels 0; Gaps 0;
Oy	394	gatgtttgaaggaccacaacctccaactcattgtgtgttacatytgaacaacgacctcc	453	
Dd	6	GGTGTAAGGAGAIGACATCATCTCCACTCTCGTGCCGCCGTCACCCTTGAGAACCGGCGCTCC	65	
Oy	454	atctcttgaagaagtcaagtcagagcgctcttgtagatgatatgaagaacatattgaattgg	513	
Dd	66	ATCTCTCTCAGAGTTATGACCAAAGCCTCCACACAGTAGTGAAMAACCTACTTGAATTGG	125	
Oy	514	ttgttaaagagagcgccagctctccaaagcgccaatcatctctgtgttctaactgac	573	
Dd	126	TTTTAGCAGAAAGCCAGGCCAATCTCCAATGAGCCCTAATTATTAAGGITTCTTACCGGGAC	185	
Oy	574	tctggagatcccctgaacaggttcaatgagtcagttgagatcacgagaaaacattcacactgaaaaatc	633	
Dd	186	TCTGGGTCGCCAAGACATTCACGCGCGAGTGCGGTACGACGACCTTCACACTGAAAATTC	245	
Oy	634	aacagatgagagcgctgaagatttggagatttatattgtctgtgcgaagatgacacattctccg	693	

[illegible][illegible]

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      80  GATATATGATGACTGACTGCTCCACTCTCCGCCGTCATCCCTGAGAGCGGCGCTC 139
      453  catctcttgcaagtcgaagtcagcctcttgatgagatgagaaagcatattgattg 512
      140  CATCTCTGCAAGTCAGTACAGAGCCCTGCTTAGTAATGATATATATTTGGATTG 199
      513  gtgttacaagagccagcagctctccaagcgccatctatctatctgtgtctaaactgga 572
      200  GTATCTGCAAGTCAGTACAGAGCCCTGCTTAGTAATGATATATATTTGGATTG 259
      573  ctcttgagtccttcagcagctcttcagcagtgatcaggagcagatttcacatgaaat 632
      260  CTCGGGGGTCCTGACAGTTCAGTGCAGTGCATGCATGATTCATTTACACTGAAAT 319
      633  caacagagtgagagctgagatgattggagttattatctgtcgcgaagtgacatctcc 692
      320  CACACAGTGTGAGGCTGAGATGTTGGGTTTACACTGATGAGGCTCTACATCTCC 379
      693  gtcacagtcgtgctggcaccacagctggaaatcaa 729
      380  TCACACTTTGGCCAGGCGACCAAGCTGAGATCAAA 416

RESULT 9
AA405415 442 bp mRNA EST 09-NOV-1997
LOCUS z56602.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone
DEFINITION IMAGE:741987 5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II
REGION (HUMAN): mRNA sequence.
ACCESSION AA405415
VERSION AA405415.1 GI:2063652
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Krizman, D., Kucaba, T., Lacey, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1053 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham.
Location/Qualifiers
1. 442
/organism="Homo sapiens"
/db_xref="GDB:5942254"
/db_xref="taxon:9606"
/clone="IMAGE:741987"
/clone_lib="Soares ovary tumor NBHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pTV73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5'
TGTTCACATCTGACATGAGCGCGCGGCTTTTATTTTATTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTV73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

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BASE COUNT 90 a 120 c 114 g 118 t
ORIGIN
Query Match 30.6%; Score 223.4; DB 7; Length 442;
Best Local Similarity 78.9%; Pred. No. 1.4e-56;
Matches 266; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

      393  ggaatgtttgatgaccacaactcactcactctgtgtgtgattacatggaacaaccctc 452
      80  GATATATGATGACTGACTGCTCCACTCTCCGCCGTCATCCCTGAGAGCGGCGCTC 139
      453  catctcttgcaagtcgaagtcagcctcttgatgagatgagaaagcatattgattg 512
      140  CATCTCTGCAAGTCAGTACAGAGCCCTGCTTAGTAATGATATATATTTGGATTG 199
      513  gtgttacaagagccagcagctctccaagcgccatctatctatctgtgtctaaactgga 572
      200  GTATCTGCAAGTCAGTACAGAGCCCTGCTTAGTAATGATATATATTTGGATTG 259
      573  ctcttgagtccttcagcagctcttcagcagtgatcaggagcagatttcacatgaaat 632
      260  CTCGGGGGTCCTGACAGTTCAGTGCAGTGCATGCATGATTCATTTACACTGAAAT 319
      633  caacagagtgagagctgagatgattggagttattatctgtcgcgaagtgacatctcc 692
      320  CACACAGTGTGAGGCTGAGATGTTGGGTTTACACTGATGAGGCTCTACATCTCC 379
      693  gtcacagtcgtgctggcaccacagctggaaatcaa 729
      380  TCACACTTTGGCCAGGCGACCAAGCTGAGATCAAA 416

RESULT 10
AM405725 488 bp mRNA EST 16-FEB-2000
LOCUS UI-HF-BL0-abv-f-05-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3057944 5', mRNA sequence.
ACCESSION AM405725
VERSION AM405725.1 GI:6924782
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
Natl. Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: M13 forward.
Location/Qualifiers
1. 488
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3057944"
/clone_lib="NIH_MGC_37"
/tissue_type="Lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/note="Vector: pTV73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA

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REFERENCE 1 (bases 1 to 911)
 AUTHORS NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Lohar Hennighausen Ph.D., Robin Humphreys
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Incey Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Plate: LHAM524 row: k column: 18
 High quality sequence stop: 688.

FEATURES

source

1. 911
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57/B6"
 /db_xref="taxon:10090"
 /clone_lib="IMAGE:3487241"
 /clone_lib="NCI-CGAP_Mam5"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: Salt; Site: 2: Not; Cloned unidirectionally. Primer: oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lohar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 190 a 262 c 261 g 197 t 1 others
 ORIGIN

Query Match 29.5%; Score 214.8; DB 106; Length 911;
 Best Local Similarity 79.2%; Pred. No. 7.2e-54;
 Matches 282; Conservative 0; Mismatches 67; Indels 7; Gaps 2;

QY 1 caggctcagctcagcagctcgtgggagagagctgtgagtcaggggagcctcagtcagtg 60
 |||||
 DB 65 CAGGTCACATGACGAGCCTGGGGCTGTGAAGCTTGAGAGCTTACGAAACCTG 124
 QY 61 tctctcagcctctctgctcctcaacatgaagactatgacactgagtgagaa-gcagag 119
 |||||
 DB 125 TCCTGCAAGGCTTCTGCTACACCTTACCAAGTTACTGATGCACTGGTGAAGCGAG 184
 QY 120 gcctgaacagggcctgagtgatgagtcagtcacccctgagaaatgtagatcagata 179
 |||||
 DB 185 GCCTGAGCAGGCGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 244
 QY 180 tgcctcagcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 229
 |||||
 DB 245 CAATGAGAACTTCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 304
 QY 240 cctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 299
 |||||
 DB 305 CATGACAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 364
 QY 300 ggaat-----gcttgcagcagcagcagcagcagcagcagcagcagcagcagcagcag 349
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 DB 365 GGATTAGAGAGCTATGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 420

RESULT 15
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 LOCUS UI-HF-BL0-scr-e-08-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 DEFINITION IMAGE:3060182 5', mRNA sequence.
 ACCESSION AM406473
 VERSION AM406473.1 GI:6925530

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 353)
 AUTHORS NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.lnl.gov/biopr/image/image.html
 Seq primer: M13 forward.

FEATURES

source

1. 353
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 /clone_lib="IMAGE:3060182"
 /clone_lib="NIH_MGC_37"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="Mc85"
 /note="Vector: p7773-Pac; Site: 1: Not; Site: 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 73 a 93 c 93 g 94 t
 ORIGIN

Query Match 29.3%; Score 213.4; DB 90; Length 353;
 Best Local Similarity 80.4%; Pred. No. 1.4e-53;
 Matches 250; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 393 ggaatgtttgattaccacaaactccactcactctgtgtgattacattggaacacagcctc 452
 |||||
 DB 43 GGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 102
 QY 453 catctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 512
 |||||
 DB 103 CATCTCTCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 162
 QY 513 gtgtgtacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 572
 |||||
 DB 163 GTACCTGACAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAGAGCAG 222
 QY 573 cctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 632
 |||||
 DB 223 CTCGGGGGCTCCGACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 282
 QY 633 caacagagtgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 692
 |||||
 DB 283 CACCAAG 342
 QY 693 gctcagcttcg 703
 |||||
 DB 343 TCACACTTCG 353

Search completed: February 18, 2001, 02:00:11
 Job time: 13895 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 18:26:59 ; Search time 96.92 Seconds
(without alignments)
2825.610 Million cell updates/sec

Title: US-09-297-181-1

Perfect score: 729
Sequence: 1 caggtcagctgcagcagctc.....gcaccagctggaatcaaa 729

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	729	100.0	729	19	V36236 DNA of SCFV 421 wh
2	717.8	98.5	768	17	T48000 Coding sequence fo
3	716.2	98.2	749	18	T86234 Anti-human protein
4	716.2	98.2	1611	18	T86221 Human p53 protein
5	505	69.3	1135	20	X58936 Plasmid pUG718 enc
6	460.8	63.2	747	19	V36237 DNA of SCFV D3M wh
7	452.2	62.0	1314	19	V09256 Nucleotide sequenc
8	435	59.7	907	20	X58690 Monoclonal antibody
9	432.2	59.3	753	20	X72745 Mouse scfv fragmen
10	432.2	59.3	810	16	O90663 MFE-23 antibody co
11	432.2	59.3	1637	21	Z88358 Bispesific anti-ze
12	429	58.8	753	20	X77241 Mouse scfv fragmen

13	425.2	58.3	1679	18	T58130
14	425.2	58.3	1679	20	V08176
15	418	57.3	726	20	X86942
16	418	57.3	726	20	X86943
17	415.2	57.0	843	20	V72069
18	415.2	57.0	1998	20	V72075
19	409.4	56.2	830	21	T61047
20	407.4	55.9	1095	18	T94969
21	407.4	55.9	1098	18	T94970
22	405.8	55.7	876	19	V10390
23	393	53.9	925	21	Z58664
24	393	53.9	925	21	Z44206
25	392	53.8	1047	20	Z21156
26	392	53.8	1086	20	Z21158
27	385.2	52.8	804	20	X78155
28	377.4	51.8	864	20	V72072
29	377.4	51.8	2019	20	V72059
30	377.4	51.8	2025	20	V72064
31	368.8	50.6	744	20	X77247
32	361.8	49.6	772	14	O35954
33	361.8	49.6	772	17	T27991
34	361.8	49.6	778	14	O35955
35	360.8	49.5	744	20	X77248
36	357.6	49.1	744	20	X77243
37	356.8	48.9	1725	20	X01651
38	354.8	48.7	732	19	V23579
39	354.8	48.7	2364	19	V23580
40	352.6	48.4	2478	20	X86614
41	352.6	48.3	720	19	V58790
42	351.6	48.2	747	13	O21098
43	349.2	47.9	1668	20	X01652
44	349.2	47.9	1797	19	V00687
45	349.2	47.9	1797	21	A10398

ALIGNMENTS

RESULT 1	
V36236	
ID V36236 standard: DNA; 729 BP.	
XX V36236;	
XX	
AC	
XX	
DT 08-SEP-1998 (first entry)	
XX	
DE DNA of SCFV 421 which binds to mutant p53 proteins.	
XX	
KX Single chain antibody; SCFV 421; mouse; p53 protein; oligomerisation;	
KW regulatory domain; p53 mutant; H273; W248; G281;	
KW p53-dependent trans-activating activity; restoration;	
KW tumour-suppressing activity; tumour cell; treatment;	
KW hyper-proliferation; cancer; re-stenosis; ss.	
XX	
OS Mus sp.	
XX	
PN W09818825-A1.	
XX	
PD 07-MAY-1998.	
XX	
PF 27-OCT-1997; 97MO-FR01921.	
XX	
PR 29-OCT-1996; 96FR-0013176.	
XX	
PA (RHON) (RHON)-POU2ENC RORER SA.	
XX	
PI Debussche L; Bracco L;	
XX	
DR WPI: 1998-272140/24.	
DR P-PSDB; W60769.	
XX	
PT Restoring p53-dependent trans-activating activity to cell containing mutant p53 - by delivering single-chain antibody specific for the	

Single chain anti-H22-anti-CEA antib
Antibody BIOC7 enc
Antibody BIOC7 com
Fusion protein PIC
Fusion protein (80
DNA encoding a sin
R. p1piens recombi
Monoclonal antibody
Antibody 4H5 L cha
Murine derived DNA
Artificial synthe
Schv4155 anti-B3G
Fusion protein PIC
Plasmid pMG4/55.1s
Fusion protein PNG
Mouse scfv fragmen
H and L chain FV r
Heavy and light ch
H and L chain FV r
Mouse scfv fragmen
Mouse scfv fragmen
Bispesific tetra
Firefly Luciferase
Antibody-Firefly l
CDNA encoding an a
scfv comprising he
pscfvMO11 encoding
Bispesific tetra
Fusion gene sequen
Recombinant DNA en


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Db      88  tccgtcacagcttctgtctcaacatnaagactactatatactgactggtgtgaagcagag 147
QY      121  cctgaacagagcctgtgagtgatgtgattgactcctgaagtgtgtactgatat 180
Db      148  cctgaacagagcctgtgagtgatgtgattgactcctgaagtgtgtactgatat 207
QY      181  gccccgaagtctcaagggcagagccactatctactgacagacacccctccataacagctac 240
Db      208  gccccgaagtctcaagggcagagccactatctactgacagacacccctccataacagctac 267
QY      241  ctgacagctcagcagcctgtgacatctgagacactgacgtcgtattattgttaattttacgg 300
Db      268  ctgacagctcagcagcctgtgacatctgagacactgacgtcgtattattgttaattttacgg 327
QY      301  gatgctttgactatgtgggccaagggacacagctacccctccctcaggttgagggcgt 360
Db      328  gatgctttgactatgtgggccaagggacacagctacccctccctcaggttgagggcgt 387
QY      361  tcagcgagagtgctgtcgtcgtgtgaggaatcgtatgtttgaatgaacccaactcactc 420
Db      388  tcagcgagagtgctgtcgtcgtgtgaggaatcgtatgtttgaatgaacccaactcactc 447
QY      421  actttgctggttaaccattggaacacacagcctcactctctgcaagtcagagcctc 480
Db      448  actttgctggttaaccattggaacacacagcctcactctctgcaagtcagagcctc 507
QY      481  ttgatatgtagtgaaagacatatattgtaattgtttgttaagaggccagggccagctccca 540
Db      508  ttgatatgtagtgaaagacatatattgtaattgtttgttaagaggccagggccagctccca 557
QY      541  aagcgccctaatctatctgtgtcgttaaacctgactgactgtgagctccctgacaggttcac 600
Db      568  aagcgccctaatctatctgtgtcgttaaacctgactgactgtgagctccctgacaggttcac 627
QY      601  agtggatcagaggaacagattcacaactgaaatacaacagagtgagggctgagagtttggga 660
Db      628  agtggatcagaggaacagattcacaactgaaatacaacagagtgagggctgagagtttggga 687
QY      661  gtttatattgtgtgcaaggttacacattcccgctcactcgttctgtgtgtgacacaaagctg 720
Db      688  gtttatattgtgtgcaaggttacacattcccgctcactcgttctgtgtgtgacacaaagctg 747
QY      721  gaaatcaaa 729
Db      748  gaaatcaaa 756

RESULT      3
ID      T86234
XX      T86234 standard; cDNA; 749 BP.
AC      T86234;
XX
DT      24-NOV-1997 (first entry)
XX
DE      Anti-human protein p53 single chain antibody ScFv 421 cDNA fragment.
XX
KW      Leucine zipper domain; LZD; oligomerisation domain; mutant; mutain;
KW      substitution; replacement; transactivation; viral protein VP16; HSV;
KW      anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
KW      tumour suppression; apoptosis; single chain antibody variable domain;
KW      ss.
XX
OS      Mammalia.
OS      Synthetic.
XX
XX      WO9704092-A1.
XX      PD      06-FEB-1997.
XX      PF      17-JUL-1996; 96WO-FR01111.
XX      PR      19-JUL-1995; 95FR-0008729.

```

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XX      (RHON ) RHONE POULENC RORER SA.
PA      Bracco L, Conseller E;
PI      WPI: 1997-132633/12.
DR
XX      New p53 variants e.g. with oligomerisation domain replaced by
PT      leucine zipper - useful for treating hyper-proliferative disorders,
PT      esp. cancer and restenosis
XX
PS      Example A; Pages 96-97; 133pp; French.
XX
CC      Claimed variants of protein p53 have at least part of the
CC      oligomerisation domain deleted and replaced by a leucine zipper
CC      domain. The mutants preferably also have at least part of the p53
CC      transactivation domain (amino acids 1-74) deleted and replaced by
CC      the transactivating domain (TD) from herpes simplex virus viral
CC      protein VP16 (amino acids 411-490) or by a protein domain able to
CC      bind selectively to a transactivator, especially a single-chain
CC      antibody variable domain (ScFv). The present sequence represents
CC      the NcoI-NcoI fragment of cDNA coding for the anti-p53 single-chain
CC      antibody ScFv 421. The fragment contains an ATG initiation codon
CC      (precise location is not indicated) and no termination codon. The
CC      p53 variants are more active and more stable tumour suppressors and
CC      apoptosis-inducing agents than wild-type p53 and are active where
CC      the wild-type protein is not, i.e. they are not inactivated by
CC      dominant negative or oncogenic mutants, nor by other cellular
CC      proteins (because the leucine zipper domain prevents formation of
CC      inactive mixed oligomers).
SQ      Sequence 749 BP; 173 A; 179 C; 221 G; 176 T; 0 other;

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Query Match      98.2%; Score 716.2; DB 18; Length 749;
Best Local Similarity 98.9%; Pred. No. 1.1e-196;
Matches 721; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1  caggtcacactgtgagagcctgtgagagcctgtgaggttcaggggccctcaatgttg 60
Db      10  caggtcacactgtgagagcctgtgagagcctgtgaggttcaggggccctcaatgttg 69
QY      61  tccgtcacagcttctgtctcaacattaaagactactatatactgacgtgtgagagag 120
Db      70  tccgtcacagcttctgtctcaacattaaagactactatatactgacgtgtgagagag 129
QY      121  cctgaacagagcctgtgagtgatgtgattgattcctcgtgaatgtgtactgatat 180
Db      130  cctgaacagagcctgtgagtgatgtgattgattcctcgtgaatgtgtactgatat 189
QY      181  gccccgaagtctcaagggcagagccactatgactgacagacacatccctccataacagctac 240
Db      190  gccccgaagtctcaagggcagagccactatgactgacagacacatccctccataacagctac 249
QY      241  ctgacagctcagcagcctgtgacatctgagacactgacgtcgtattattgttaattttacgg 300
Db      250  ctgacagctcagcagcctgtgacatctgagacactgacgtcgtattattgttaattttacgg 309
QY      301  gatgctttgactatgtgggccaagggacacagctacccgtcctcctcaggtgagggcgt 360
Db      310  gatgctttgactatgtgggccaagggacacagctacccgtcctcctcaggtgagggcgt 369
QY      361  tcagcgagagtggtcctgtggtgtgaggaatcgtatgtttgatgacccaactcactc 420
Db      370  tcagcgagagtggtcctgtggtgtgaggaatcgtatgtttgatgacccaactcactc 429
QY      421  actttgctggttaaccattggaacacacagcctcactctctgcaagtcagagcctc 480
Db      430  actttgctggttaaccattggaacacacagcctcactctctgcaagtcagagcctc 489
QY      481  ttgatatgtagtgaaagacatatattgtaattgtttgttcaagggccagggccagctccca 540
Db      490  ttgatatgtagtgaaagacatatattgtaattgtttgttcaagggccagggccagctccca 549

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QY 541 aagcgccatctatctggtgtctaaactgagcttgagctccctgacaggttcaactgagc 600
 |||||
 Db 550 aagcgccatctatctggtgtctaaactgagcttgagctccctgacaggttcaactgagc 609
 QY 601 agtgcagcagggagagatcttcaactcaaaatcaacagagtgagagcttgagattggga 660
 |||||
 Db 610 agtgcagcagggagagatcttcaactcaaaatcaacagagtgagagcttgagattggga 669
 QY 661 gttattattgctgcaagagatcttccgctcagcttgagcttgagcagcaagctg 720
 |||||
 Db 670 gttattattgctgcaagagatcttccgctcagcttgagcttgagcagcaagctg 729
 QY 721 gaaatcaaa 729
 |||||
 Db 730 gagctgaaa 738
 RESULT 4
 ID T86221 standard; cDNA: 1611 BP.
 XX T86221;
 AC T86221;
 DT 24-NOV-1997 (first entry)
 XX Human p53 protein variant S-325 coding sequence from pEC176.
 DE
 XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutuin;
 KM substitution; replacement; transactivation; viral protein VP16; HSV;
 KM anti-oncogene; hyperproliferation; cancer; restenosis; SCFV;
 KM tumour suppression; apoptosis; single chain antibody variable domain;
 SS.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Herpes simplex virus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1611
 FT /*tag- a
 FT /product= S-325
 FT /note= "Open reading frame ends with two tandem
 termination codons"
 FT
 XX
 PN M09704092-A1.
 XX
 PD 06-FEB-1997.
 XX
 PF 17-JUL-1996; 96WO-FR01111.
 XX
 PR 19-JUL-1995; 95FR-0008729.
 XX
 PA (RHON) RHONE POULENC ROBER SA.
 XX
 PI Bracco L, Conseiller E;
 XX
 DR WPI; 1997-132633/12.
 XX
 DR P-PSDB; W28491.
 XX
 PT New p53 variants e.g. with oligomerisation domain replaced by
 leucine zipper - useful for treating hyper-proliferative disorders,
 esp. cancer and restenosis
 XX
 PS Claim 42: Pages 88-90; 133pp. French.
 XX
 CC Claimed variants of protein p53 have at least part of the
 CC oligomerisation domain deleted and replaced by a leucine zipper
 CC domain. The mutants preferably also have at least part of the p53
 CC transactivation domain (amino acids 1-74) deleted and replaced by
 CC the transactivating domain (TD) from herpes simplex virus viral
 CC protein VP16 (amino acids 411-490) or by a protein domain able to
 CC bind selectively to a transactivator, especially a single-chain

CC antibody variable domain (SCFV). The present sequence encodes
 CC a specifically claimed p53 variant designated S-325 and comprising
 CC a SCFV domain, amino acids 75-325 of human wild-type p53 and a
 CC leucine zipper domain at the C-terminal. The p53 variants are
 CC more active and more stable tumour suppressors and apoptosis-inducing
 CC agents than wild-type p53 and are active where the wild-type protein
 CC is not, i.e. they are not inactivated by dominant negative or oncogenic
 CC mutants, nor by other cellular proteins (because the leucine zipper
 CC domain prevents formation of inactive mixed oligomers).
 XX
 SQ Sequence 1611 BP; 369 A; 443 C; 458 G; 341 T; 0 other;

Query Match 98.2%; Score 716.2; DB 18; Length 1611;
 Best Local Similarity 98.9%; Pred. No. 1,5e-196;
 Matches 721; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 caggtgcagctgcagcagctctggtggcagagctgtgagtcagggcctcagcaggtg 60
 |||||
 Db 7 caggtgcagctgcagcagctctggtggcagagctgtgagtcagggcctcagcaggtg 66
 QY 61 tctctgcagagctctggtctcaacattaaagactactatgtgactgggtggaagcagag 120
 |||||
 Db 67 tctctgcagagctctggtctcaacattaaagactactatgtgactgggtggaagcagag 126
 QY 121 cctgaacagggcctggaagtgtgattgattgattgattgattgattgattgattgatt 180
 |||||
 Db 127 cctgaacagggcctggaagtgtgattgattgattgattgattgattgattgattgatt 186
 QY 181 gccccgaagctccagggcagggccactatgactgcagacacatccccaatcaccttac 240
 |||||
 Db 187 gccccgaagctccagggcagggccactatgactgcagacacatccccaatcaccttac 246
 QY 241 ctgcagctcagcagcctggtgacttgagagacactgcccctctattgtgatttttcaggg 300
 |||||
 Db 247 ctgcagctcagcagcctggtgacttgagagacactgcccctctattgtgatttttcaggg 306
 QY 301 gatgcttgagctatttggggcagagggacacagctcctcctcaggtgagggcgggt 360
 |||||
 Db 307 gatgcttgagctatttggggcagagggacacagctcctcctcaggtgagggcgggt 366
 QY 361 tcagcgagaggtggtcctggtggtggtggtggtggtggtggtggtggtggtggtggt 420
 |||||
 Db 367 tcagcgagaggtggtcctggtggtggtggtggtggtggtggtggtggtggtggtggt 426
 QY 421 acttgctggttacattgagacacagcctccatctcttgcagagtcagagtcagcctc 480
 |||||
 Db 427 acttgctggttacattgagacacagcctccatctcttgcagagtcagagtcagcctc 486
 QY 481 ttgagatgagtggaagacacatatgtgaattgtgttacaagggcagggccagcttcca 540
 |||||
 Db 487 ttgagatgagtggaagacacatatgtgaattgtgttacaagggcagggccagcttcca 546
 QY 541 aagcgccatctatctggtgtgttaactgagcttgagagctccctgacaggttcaactgagc 600
 |||||
 Db 547 aagcgccatctatctggtgtgttaactgagcttgagagctccctgacaggttcaactgagc 606
 QY 601 agtgcagcagggagagatcttcaactcaaaatcaacagagtgagagcttgagattggga 660
 |||||
 Db 607 agtgcagcagggagagatcttcaactcaaaatcaacagagtgagagcttgagattggga 666
 QY 661 gttattattgctgcaagagatcttccgctcagcttgagcttgagcagcaagctg 720
 |||||
 Db 667 gttattattgctgcaagagatcttccgctcagcttgagcttgagcagcaagctg 726
 QY 721 gaaatcaaa 729
 |||||
 Db 727 gagctgaaa 735
 RESULT 5
 ID X58936 standard; DNA: 1135 BP.

XX	
AC	X58936;
DF	23-AUG-1999 (first entry)
DE	Plasmid pJG718 encoding scFv A77-PDGR-R TM fusion.
KM	Single chain antibody; scFv; A77; IGA receptor; Fc receptor; Fc alpha receptor; platelet derived growth factor receptor; KX tumour engineering; cell surface expression; therapy; cancer; XX tumour; vaccine; human; ds. XX XX OS Chimeric - Mus sp. OS Chimeric - synthetic. XX XX Key Location/Qualifiers FT 74..1135 FT CDS /*tag= a FT FT PN MO928349-A2. PD 10-JUN-1999. XX XX 02-DEC-1998; 98WO-US25556. PF PR 02-DEC-1997; 97US-0067232. XX PA (MEDA-) MEDAREX INC. XX XX Deo YM, Goldstein J, Graziano R, Keler T; DR WPI: 1999-DRI099/31. DR P-PSDB; Y06273. XX XX Cells expressing anti-Fc receptor binding components XX XX Example 6; Fig 10A-E; 68pp; English. CC This is the DNA sequence of a portion of vector pJG718 that codes CC for a fusion protein (see Y06273) comprising murine anti-Fc alpha CC receptor antibody A77 sFv and the transmembrane domain of platelet CC derived growth factor receptor (PDGR-R TM). pJG718 expression CC vector was constructed by inserting a DNA segment encoding the A77 CC sFV in frame with the PDGR-R TM sequence in plasmid vector pDisplay. CC Murine tumour cells transformed to express A77-TM were able to bind CC a soluble form of the Fc alpha receptor, and the bound receptor was CC able to engage IgA molecules. This is an example of cells of the CC invention that have been transformed to express on their surface a CC component which binds to an Fc receptor of an effector cell. The CC transformant cell is targeted to an effector cell via the Fc binding CC component, and can be used as a vehicle to increase an effector CC cell-mediated immune response, such as cell lysis and phagocytosis, CC against an antigen associated with the cell. The transformed cells CC are used to treat cancer and infectious diseases or used as CC vaccines. The method allows for killing of target cells without CC targeting any particular antigen on the cell. This is advantageous CC since many tumour cells and other target cells do not have defined CC antigens for targeting. XX XX Sequence 1135 BP; 274 A; 273 C; 310 G; 278 T; 0 other; XX

	Query Match	69.3%	Score 505	DB 20	Length 1135
	Best Local Similarity	81.2%	Pred. NO. 7.2e-136		
	Matches 608	Conservative 0	Mismatches 120	Indels 21	Gaps 14
QY	2 aggtgcagctgcagcagcctctgggcagagactgttgaagtcacaggccctacacgaattgt	61			
DB	186 agatccacctgcagcagcagcttgccttgcagcttgcgtgaagctctgggcttcacggaagatat	245			
QY	62 cctgcacagctctctggcttcacacttaagaactatattatgcacgggggtggaagcagagcc	121			
DB	246 cctgcgaagctctctggttatctatcattcactgcattacatcatctatttggggggaagcagagcc	305			

[illegible]

RESULT	6	
ID	V36237	
	V36237 standard; DNA; 747 BP.	
AC	V36237;	
DT	08-SEP-1998	(first entry)
DE	DNA of SCFV D3M, which binds to mutant p53 proteins.	
XX		
XX	Single chain antibody; SCFV D3M; mouse; p53 protein; oligomerisation;	
KM	regulatory domain; p53 mutant; H273; W248; G281;	
KW	p53-dependent trans-activating activity; restoration;	
KW	tumour-suppressing activity; tumour cell; treatment;	
XX	hyper-proliferation; cancer; re-stenosis; ss.	
OS	Mus sp.	
XX		
PN	WC0818825-A1.	
XX		
PD	07-MAY-1998.	
XX		
PF	27-OCT-1997;	97MO-FR01921.
XX		
PR	29-OCT-1996;	96FR-0013176.
XX		
PA	(RHON) RHONE-POULENC ROBER SA.	

XX Debussche L, Bracco L;
 XX
 XX WPI: 1998-272140/24.
 DR P-PSDB; W60770.
 XX
 PT Restoring p53-dependent trans-activating activity to cell containing
 PT mutant p53 - by delivering single-chain antibody specific for the
 PT mutant, particularly for treatment of tumours
 XX
 PS Claim 5; Page 32; 54pp; French.
 XX
 CC The present sequence encodes a single chain antibody (ScFv) designated
 CC DJM. The antibody binds to an epitope present in the C-terminal region
 CC of the p53 protein that includes oligomerisation and regulatory domains,
 CC specifically between positions 320 and 393. ScFv DJM is directed against
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
 CC introduced into cells containing a mutant p53 protein, p53-dependent
 CC trans-activating activity is restored. ScFv DJM is specific for
 CC p53-mutants that have lost tumour-suppressing activity and are present in
 CC tumour cells. It is particularly used to treat hyper-proliferation
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant
 CC and to purify or detect p53.
 XX
 SQ Sequence 747 BP; 189 A; 188 C; 205 G; 165 T; 0 other;

Query Match 63.2%; Score 460.8; DB 19; Length 747;
 Best Local Similarity 79.2%; Pred. No. 3,2e-123;
 Matches 594; Conservative 0; Mismatches 132; Indels 24; Gaps 3;

QY 1 caggtgagctgagcagctctggtgagcagctgtgagcaggggctcagtcagtg 60
 DB 1 caggtgagctgagcagctctggtgagcagctgtgagcaggggctcagtcagtg 60
 QY 61 tctgtccagctctgtgctcacaataaagcactacatgtgctggtgagcagag 120
 DB 61 tctgtccagctctgtgctcacaataaagcactacatgtgctggtgagcagag 120
 QY 121 ccggaagagcctggtgagtgatgtgattgctcagagatggtgagtgatgaat 180
 DB 121 ccggaagagcctggtgagtgatgtgattgctcagagatggtgagtgatgaat 180
 QY 181 gccccgaagctcagagcagagccactatgactgacagacatcctccaaacagc 240
 DB 181 gccccgaagctcagagcagagccactatgactgacagacatcctccaaacagc 240
 QY 241 ctgagctcagcagcctgctgctgacatctgagacacgctcattatgtat 291
 DB 241 ctgagctcagcagcctgctgctgacatctgagacacgctcattatgtat 291
 QY 292 -----tttacaaggagtgctgcttgactatgtgggccaaggagacagctgc 342
 DB 292 -----tttacaaggagtgctgcttgactatgtgggccaaggagacagctgc 342
 QY 301 tactatgataagcagcgtctgtcttgactactggtggccaaggagacagctgc 360
 DB 301 tactatgataagcagcgtctgtcttgactactggtggccaaggagacagctgc 360
 QY 343 tctcaggtgagcagctcagcagcagagctgctgctgagcagtgatcgatgtt 402
 DB 343 tctcaggtgagcagctcagcagcagagctgctgctgagcagtgatcgatgtt 402
 QY 361 tctcaggtgagcagctcagcagcagagctgctgctgagcagtgatcgatgtt 420
 DB 361 tctcaggtgagcagctcagcagcagagctgctgctgagcagtgatcgatgtt 420
 QY 403 atgacccaactcactcaacttctgtcgtgtacacatgagaaacacagctccttc 462
 DB 403 atgacccaactcactcaacttctgtcgtgtacacatgagaaacacagctccttc 462
 QY 421 ctacccagctcactcacttccctgctgtgtcagcagagagagagctcgtatgag 480
 DB 421 ctacccagctcactcacttccctgctgtgtcagcagagagagagctcgtatgag 480
 QY 463 aagtcagatcagagcctcttggga---tagtgatgaaagacatattgattgtgt 519
 DB 463 aagtcagatcagagcctcttggga---tagtgatgaaagacatattgattgtgt 519
 QY 481 aaatccagtcagagctgtgtcacaagtagaaccgaaagattactgtgctgtatcg 540
 DB 481 aaatccagtcagagctgtgtcacaagtagaaccgaaagattactgtgctgtatcg 540
 QY 520 cagaagcagcagctcacaagcgcctaatctatctgctcctaactgagctcctg 579
 DB 520 cagaagcagcagctcacaagcgcctaatctatctgctcctaactgagctcctg 579
 QY 541 cagaagcagcagctcctaactgctcctaactgctcctaactgagctcctgag 600
 DB 541 cagaagcagcagctcctaactgctcctaactgctcctaactgagctcctgag 600
 QY 580 gtccctgacagctcagctgagcagtgatcagagacagattcactgaataacacaga 639
 DB 580 gtccctgacagctcagctgagcagtgatcagagacagattcactgaataacacaga 639

DB 601 gtccctgagctcagcagcagtgatcctggtgagcagattcactcaccacagcag 660
 QY 640 gtgagagctgagagcttggagatttattgtctggaagctacacattccgcagcag 699
 DB 661 gtgagagctgagagcttggagatttattgtctggaagctacacattccgcagcag 717
 QY 700 ttcggtgctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 729
 DB 718 ttcggtgctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 747

RESULT 7
 ID V09256 standard; CDNA; 1314 BP.
 AC V09256;
 DT 07-JUL-1998 (first entry)
 XX
 DE Nucleotide sequence encoding the Mgr6-clavin immunotoxin.
 XX
 KW Recombinant ribosomal inhibitor protein; RIP; clavin; inhibition; ss;
 KW protein synthesis; conjugate; Mgr6-clavin; anticancer; antiviral agent
 KW fusion protein; chimeric.
 OS Chimeric - Mus musculus.
 OS Chimeric - Aspergillus clavatus.
 FH Key Location/Qualifiers
 FT CDS 1..1314
 FT FT /tag= a
 FT FT /product= "Mgr6-clavin immunotoxin"
 FT FT 108..861
 FT FT /tag= b
 FT FT /product= "Single Fv of Mgr6"
 FT FT /note= "derived from M. musculus"
 FT FT 861..1314
 FT FT /tag= c
 FT FT /product= "Clavin"
 FT FT /note= "derived from A. clavatus"
 PN W09749726-A1.
 PD 31-DEC-1997.
 XX
 PF 26-JUN-1997; 97WO-EP03359.
 XX
 PR 27-JUN-1996; 96IT-FI00155.
 XX
 PA (ITUV-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
 XX
 PI Colnaghi M, De Santis R, Mele A, Parente D;
 XX
 DR WPI: 1998-077109/07.
 DR P-PSDB; W377738.
 PT DNA encoding Aspergillus clavatus-derived ribosomal inhibitor
 PT protein, clavin - useful as an immuno-conjugate and for treatment of
 PT cancer
 PS Claim 3; Page 13; 26pp; English.
 XX
 CC This nucleotide sequence encodes a fusion protein comprising of the
 CC Mgr6 single chain antibody (with the heavy and light chain joined
 CC by a linker), fused to the clavin protein. Clavin is an inhibitor
 CC protein, and functions by inactivating the ribosomes. Clavin or its
 CC conjugates are useful as anticancer and/or antiviral agents. The
 CC recombinant ribosomal inhibitor protein (RIP), Mgr6-clavin (a conjugate
 CC of clavin) is used as an immunoconjugate, and the complex and clavin
 CC alone are capable of inhibiting ribosomal activity.
 XX
 SQ Sequence 1314 BP; 338 A; 360 C; 359 G; 257 T; 0 other;

Db	96	aagctgacgctgtgtgagctgctcgtgggagagcgtcgaagtgcagcttgtaggggtcccttgaactct	155
Qy	62	cctgcacagctctcgtccttccaacatlaaagactacataatgcactcgtgggtcgaagcagaagc	121
Db	156	cctgtgcacacccctcttgattccaattccaatactacacagcgcatgcttctgtgttcgcgacatc	215
Qy	122	ctgaaacagggcctggagcttgattgtagtgcgtatctccctggaaatggctgatactgaatatg	181
Db	216	cagacacagagcgtcgtgagctgtgctgcacacctatataatgtaattgtgtctcaactttatg	275
Qy	182	ccccgaagcttccagggcgaagggccactatgactcgcagacacacatccccaatacagccctacc	241
Db	276	cagacacagcttgtaagggccgcatlccacattccagagacaatgcacaaataaacaccctgtatc	335
Qy	242	tgcagctcgcgaacccctggactcgtgagagacacctcgcctctatcttgaatttttaagggg	301
Db	336	tgcacaatgacacagccggaagctcggggagacccagggcatgctatctcgtgtgaagsgatata	335
Qy	302	atgccttgtagctattctgtgggccaaggggacccaagctcaccgctctccatcctcaggtgagagcggt	361
Db	396	gtaattacgctcgtcgtgggccaaggggcgctgtgctcaactgctcctagtggtgagggcggtt	455
Qy	362	cagggcgagagctgtgctcgtcgtgtgcgagatcg---gatgttttgatgacccaatccac	418
Db	456	cagggcgagagctgtgacagcggcggtgycggatcgtctatgattctgtgatacccaatccac	515
Qy	419	tcaacttgcggttaccatcttgagacaacccaagcctccatctcttcgaagtaagtaagcagaac	478
Db	516	tcaacttgcggttaccatcttgagacaacccaagcctccatctcttcgaagtaagtaagcagaac	575
Qy	479	tcttggaatagctgatacgtgaaagacatattgaattggttctacaagagccagggccagcttc	538
Db	576	tcttggaatagctgatacgtgaaagacatattgaattggttctacaagagccagggccagcttc	635
Qy	539	caaaagcgcctaattctatctcgtgtctcacaactggacccctggagcccttgaaagtttaactg	598
Db	636	caaaagcgcctaattctcctcgtgtctcacaactggacccctggagcccttgaaagtttaactg	695
Qy	599	gcagctgacacaggaacagatttccacactgaaataacacagagctgagagctcgaagatttgg	658
Db	696	gcagctgacacaggaacagatttccacactgaaataacacagagctgagagctcgaagatttgg	755
Qy	659	ggagttattatctgcctgcgaagaggaacacattctccgtcaccagttcggctgcggaccaaagc	718
Db	756	ggagttattatctgcctgcgaagaggaacacattctccgtcaccagttcggctgcggaccaaagc	815
Qy	719	tggaaatcaca 729	
Db	816	tggagctgaaa 826	
RESULT 9			
X77245			
X77245 standard; DNA; 753 BP.			
X77245:			
DT	04-AUG-1999	(first entry)	
XX	Mouse scfv fragment 4-7 encoding DNA.		
XX	Binding site domain: BSD: epitope: fusion protein; therapeutic; cancer		
KW	autoimmune disease; scfv-antibody; single-chain Fv; mouse; ss.		
OS	Mus sp.		
XX	W03925818-A1.		
PN	27-MAY-1999.		
XX	16-NOV-1998; 98WO-EP07313.		
XX			

XX 17-NOV-1997; 97EP-0120096.
PA (KUEF/) KUFER P.
XX Borschert K., Kufer P., Lutterbuese R., Raum T., Zettl F;
FI WPI: 1999-338004/28.
DR P-PDSB; Y17962.
XX
XX
PT Phage display system for identification of binding site domains retaining capacity to bind an epitope
PT
PS Disclosure; Fig 6.8; 152pp; English.
XX
CC The invention relates to a method of identifying binding site domains (BSD) that retain the capacity of binding to a predetermined epitope when positioned C-terminal of at least one further domain in a recombinant bi- or multivalent polypeptide. The method comprises (a) testing a panel of BSD displayed on the surface of a biological display system as part of a fusion protein for binding to a predetermined epitope, where the fusion protein comprises an additional domain positioned N-terminal of the BSD and an amino acid sequence that mediates anchoring of the fusion protein to the surface of the display system; and (b) identifying a BSD that binds to the predetermined epitope. The method is useful to identify bi- or multivalent polypeptides that comprise antibody binding sites capable of efficiently binding to the corresponding antigen. The polypeptides or antibodies identified by the method are useful therapeutically and diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody fragments that bind independently of their position within bifunctional single-chain fusion proteins can be isolated from combinatorial antibody libraries using the new in vitro method. Sequences x77240-248 represent DNA sequences encoding mouse scFv fragments.

Sequence 753 BP; 171 A; 188 C; 215 G; 179 T; 0 other;

Query Match	Similarity	Score	432.2	DB	20	Length	753
Best Local	561	Conservative	75.3%	Pred.	NO.5.4e-115	Indels	21
Matches	561	Conservative	0	Mismatches	163	Indels	21
						Gaps	1
QY	6	gcacgtcgcaacatctcgggagcagagctcttgagctcagagcgccctcaagcttgcctc	65				
Db	9	gctgcttcgagcaatctcggagctgagctgagctgagcgcttgagcttcagtgagagctgctc	68				
QY	66	cacagctctctgagcttcaacattaaagactatatagtcactggtggtgaaagcagagcgctga	125				
Db	69	caagagcttcctcggtacacatctcacaacatctatgttttaagcttggtgaaagcagagcgctbg	128				
QY	126	acagagcgctgagatgatttgatgattgattcctctgaagaatggttgatataatgatgcccc	185				
Db	129	acaggtctcttgagatgatttgagagagtttatctatctgaagtgttgaaatggtcttccaaatga	188				
QY	186	gaagttccagggcgaagggccacatgatgacgcagacacatccccaataagactacctcgca	245				
Db	189	gaagttccaaagggaagagccacacagctgcgcagacaacatccccaagcagagcgctccatgga	248				
QY	246	gctccagcagagccttcgacatctcgagagacactgcgctccattatg-----	287				
Db	249	gctccagcagagccttcgacatctcgcagagaccttcgcttcattctctgtaagaagcgggatcccta	308				
QY	288	-----taatttttacagggatagctcttggaactataggggccaagagagacacagctcacgctctc	344				
Db	309	cgatactaaactaagactatgtaactcgaatgctctcgaggccaagagagacacagctcacgctctc	368				
QY	345	ctcaggttgagagcggtgtcaagcgcgaggtgagctctgacgttgagcgatctgagtttgat	404				
Db	369	ctcaggttgaggtggtgtcttcgagcgagcgagcctccggttgaggttggtcttgagctcgagat	428				
QY	405	gacacaaactccactactcttggttcaacatgttgagacacacgctccatctcttgca	464				
Db	429	gaccacgaactccactctccctgcctctcagcttggtgagataaagcctccatctcttcag	488				
QY	465	gtcaagtcagagagcctcttgatagatgagtgaaagacatatattgatttgatggtgtatagag	524				

DB 489 atctagtcagacccctgtctacacagtaacacacacatttactgtgtactctgcagaa 548
OY 525 gccacgacagctccaaagcgccttaattctgtgtctaacgagctcggagctcc 584
DB 549 gccacgacagctccaaagcgccttaattctgtgtctaacgagctcggagctcc 608
OY 585 tcacaggttctactgagctgagtcagagacagattccacactgaataacacagagtgaa 644
DB 609 agacaggttctactgagctgagtcagagacagattccacactgaataacacagagtgaa 668
OY 645 ggcctgagatttggagatttatttctgtgcagaggtacacatttcgcgtcagctgg 704
DB 669 ggcctgagatttggagatttatttctgtgcagaggtacacatttcgcgtcagctgg 728
OY 705 tgcctgacacacagctggaataaa 729
DB 729 aggggggacacagcttgagataaa 753

RESULT 10
O90663
ID O90663 standard; DNA: 810 BP.
AC Q90663:
XX 26-JAN-1996 (first entry)
XX MFE-23 antibody coding sequence.
DE MFE-23 antibody coding sequence.
KW Antibody; MFE-23; carcinoembryonic antigen; CEA; colorectal tumour;
XX therapy; diadody; ds.
OS Mus musculus.
XX Key Location/Qualifiers
FH misc_feature 79..438
FT /*tag= a
FT /*note= "variable heavy chain"
FT misc_feature 439..483
FT /*tag= b
FT /*note= "linker region"
FT misc_feature 484..801
FT /*tag= c
FT /*note= "variable light chain"
XX W09515341-A1.
XX 08-JUN-1995.
XX 05-DEC-1994; 94WO-GB02658.
XX 03-DEC-1993; 93GB-0024807.
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX Begent RHJ, Chester KA, Hawkins RE;
XX WPI; 1995-215234/28.
XX P-PsDB; R75719.
XX Antibody for carcinoembryonic antigen - for treatment and diagnosis
XX of colorectal cancer
XX Claim 3; Page 48-49; 72pp; English.
XX PS
XX This sequence represents the coding sequence for the MFE-23 antibody.
XX The encoded protein is an antibody against carcinoembryonic antigen
XX (CEA). CEA is a marker antigen for cancer imaging and therapy. The
XX MFE-23 antibody sequence was obtained using phage technology. In this
XX process, mice were immunised with CEA. The antibody variable region
XX genes obtained from these mice were then amplified from cDNA and cloned
XX as a single chain Fv (scFv) into bacteriophage vectors, producing a

CC library. The phages that bound to biotinylated CEA were selected and
CC amplified, and this sequence (and the protein it encoded) were selected.
CC The MFE-23 antibody was found to have good specificity and affinity for
CC CEA, meaning that it can be used in targeted anti-tumour therapies. A
CC humanised antibody with the complementary determining regions of MFE-23
CC may be made by CDR grafting. The antibody may be used for the treatment
CC by surgery or therapy of a colorectal tumour, or in the diagnosis of a
CC colorectal tumour. MFE-23 may also be used to make diadodies (bivalent
CC or bispecific antibody fragments which bind to two different antigens),
CC and may be linked to an antitumour agent or a detectable label.
XX
SQ Sequence 810 BP; 189 A; 220 C; 222 G; 179 T; 0 other:
Query Match 59.3%; Score 432.2; DB 16; Length 810;
Best Local Similarity 76.7%; Pred. No. 5.5e-115;
Matches 568; Conservative 0; Mismatches 143; Indels 30; Gaps 2;
OY 1 caggtcagctgcagcagctcgtgcagagctgtgagtcaggggcccacagtcagtg 60
DB 79 caggtgaaactgcagcagctcgtgcagagctgtgagtcaggggcccacagtcagtg 138
OY 61 tctctcagcgtctgtgtctcaacataaagactactatgtacactggtggaagcagag 120
DB 139 tctctcagcgtctgtgtctcaacataaagactactatgtacactggtggaagcagag 198
OY 121 cctgacagggcctggaagtgatgagtgatgacatcctggaagtgatgacatgaaat 180
DB 199 cctgacagggcctggaagtgatgagtgatgacatcctggaagtgatgacatgaaat 258
OY 181 gccccgaagctccagggaggaagccactatgactcagacacacatcctccacacagctac 240
DB 259 gccccgaagctccagggaggaagccactatgactcagacacacatcctccacacagctac 318
OY 241 ctgcagctcagcagcctgagctcgtgaggaacactgcgtctatttgaat----- 291
DB 319 ctgcagctcagcagcctgagctcgtgaggaacactgcgtctatttgaatgagggagct 378
OY 292 ---tttaagggtgactgtgactatggggcgaaggagacaggtacagctctccca 348
DB 379 cagactggcggtaactctgactcagcaggggccaaggagacaggtacagctctccca 438
OY 349 ggtgagagcgggttcagggcggaggtgctcgtgcgtgcggatcgatgtttgatgac 408
DB 439 ggtgagagcgggttcagggcggaggtgctcgtgcgtgcggatcgatgaaatggtctcc 498
OY 409 caactcactcactgtgtcgttacatcagacacacagcctccatctctgcaagtca 468
DB 499 agtctcagacatcgtgtcgttacatcagacacacagcctccatctctgcaagtca 558
OY 469 agtctcagacatcgtgtcgttacatcagacacacagcctccatctctgcaagtca 528
DB 559 agtctcagacatcgtgtcgttacatcagacacacagcctccatctctgcaagtca 600
OY 529 gccacgtctccaaagcgccttaattctgtgtctaaactggaactggagctccctac 588
DB 601 gccacgtctccaaagcgccttaattctgtgtctaaactggaactggagctccctac 660
OY 589 aggttactgagctgagtcagagacagattccacactgaataacacagagtgagagct 648
DB 661 cgttcagtgagagtgagtcagagacagattccacactgaataacacagagtgagagct 720
OY 649 gaggttggaggttattatgtctggaagagtgacacttccgcgtcagctgagct 708
DB 721 gaggttggaggttattatgtctggaagagtgacacttccgcgtcagctgagct 780
OY 709 gccacacagctggaataaa 729
DB 781 gccacacagctggaataaa 801

RESULT 11
288358

ID 288358 standard; DNA; 1637 BP.
 AC 288358;
 DT 04-MAY-2000 (first entry)
 DE Bispecific anti-zeta-chain/anti-EpCAM antibody nucleotide sequence.
 XX Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
 KW complementary determining region; CDR; autoimmune disease; cytostatic;
 KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
 KW immunosuppressive; antimicrobial; immune response modulator; NK-cell; ds.
 XX
 OS Rattus norvegicus.
 SN Synthetic.
 PN WO200003016-A1.
 XX
 XX 20-JAN-2000.
 PD
 PF 09-JUL-1999; 99WO-EP04838.
 PR 10-JUL-1998; 98EP-0112867.
 XX
 PA (CONN-) CONNEX GMBH.
 XX
 XX Reiter C;
 PI
 DR WPI: 2000-160926/14.
 DR P-PSDB: Y78328.
 PT
 PT New oligonucleotide, polypeptide, antibody useful for treating
 PT autoimmune disease, immune deficiencies, T-cell malignancies and
 XX infectious diseases.
 XX
 PS Example 9; Page 74; 79pp; English.
 XX
 XX The present invention describes a nucleic acid molecule (I) encoding at
 CC least one complementary determining region (CDR) of a variable region of
 CC antibody which specifically interacts with the extracellular domain of
 CC the human zeta-chain. The antibody whose CDR of a variable region is
 CC encoded by (I), is obtained by immunising a rat with jurkat cells and
 CC subsequently with a conjugate comprising a carrier molecule and a
 CC peptide having an N-terminal amino acids of a rat zeta-chain. The
 CC anti-zeta-chain antibody is useful for the treatment and prevention of
 CC autoimmune diseases, immune deficiencies, T-cell malignancies,
 CC infectious diseases and the suppression of immune response preferably in
 CC order to avoid graft rejection after organ transplantation, malignancies,
 CC or viral infections. The antibody, and fragments of it, can be useful for
 CC the enhancement or suppression of NK-cell dependent immunity or for the
 CC treatment of NK-cell derived malignancies. It can also be useful for the
 CC determination of zeta-chain or eta-chain expression on NK-cells,
 CC T-lymphocytes or their precursors. The present sequence encodes a
 CC bispecific anti-zeta-chain/anti-EpCAM antibody, from an example from
 CC the present invention.
 XX
 XX Sequence 1637 BP; 398 A; 404 C; 436 G; 399 T; 0 other;

Query Match	59.3%	Score 432.2	DB 21	Length 1637
Best Local Similarity	75.3%	Pred. No. 7	1e-115	
Matches	561	Conservative	0	Mismatches 163
				Indels 21
				Gaps 1
OY	6	gcacgtcagcagcagctctgggacagactctgtatgagtcagagggccctccagtcagattgtctcg	65	
Db	825	gctcgtcagcagcagctctggagctgagctggcagagggccctgggctcttcagttgaactgtctcg	884	
OY	66	cacacgtcttcgcttccaacattaaagacactatagcacttggtgttaaacagaagggcctca	125	
Db	885	caaggtcttcgtgctcaccttcacaaactatggtttaagctgggtgaagcagaagggccctgg	944	
OY	126	acaaaggcctggagctgagatgtatgtatgattatctcttgagaatgtgtatcactgtaatatgcccc	185	

Db	945	acaagctcttgatggtatggaagatgttatctactagattgtaagtcttactacaatga	1004
Oy	186	gaattctcaaggcaagagccacatatgactcacaacacatccccaatcaagctacacgca	245
Db	1005	gaattctcaagagcaagagcccaactgactcagcaacaacatccccaagcaacagctccaatga	1064
Oy	246	gctcagaagacgttgacatctcgaagacactgcgcctcatatattg-----	287
Db	1065	gtctcgaagccttgactacctcgaagacactcgcgtctcattcttcgtgcaagagcggaatccta	1124
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Db	1125	cgatactcaaacgaagactggttaacttcgatatgtctcggggccaagaggaaccaagctacacgtctc	1184
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Oy	465	gtcaatgcacaagcctctcttgatagatgagatgaaagacatatattgattggtttacagag	524
Db	1305	atcctagctcaagatcctgtgtaacacagtaatgaaacccatttaactgtgtaaccctgcagaa	1364
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Oy	585	tgacaagttcactctgcagatgagatcagaaggaacagattccacatctgaaatacaacagatgga	644
Db	1425	agaacaggttctactgtgcagatgagatcagaaggaacagattccacatctgaaatacaacagatgga	1484
Oy	645	ggctcgaagatttggaagttattattatgctcgggaaggtacacatctccgcgtcaagttcgg	704
Db	1485	ggctcgaagatttggaagttattattatgctcgaaggtacacatctccgcgtcaagttcgg	1544
Oy	705	tgctcggcacccaagctggaatacaaa	729
Db	1545	agggggggaaccaagcttgagatcaaa	1569
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X77241	ID	X77241 standard: DNA: 753 BP.	
XX	AC	X77241;	
XX	DT	04-AUG-1999 (first entry)	
XX	DE	Mouse scFv fragment 3-5 encoding DNA.	
XX	OS	Mus sp.	
XX	PN	W09925818-A1.	
XX	PD	27-MAY-1999.	
XX	PF	16-NOV-1998; 98MO-BP07313.	
XX	FR	17-NOV-1997; 97EP-0120096.	
XX	PA	{KUFE/} KUFEF P.	
XX	PI	Borschelt K, Kufer P, Lutterbuese R, Raum T, Zettl F;	
XX	DR	WPI; 1999-338004/28.	
XX	RR	P-PSDB; YI/958.	

RESULT	12
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XX	XX77241 standard; DNA; 753 BP.
XX	
AC	XX77241;
XX	
DT	04-AUG-1999 (first entry)
DE	
XX	Mouse scFv fragment 3-5 encoding DNA.
XX	
KW	Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer
KW	autoimmune disease; scFv-antibody; single-chain Fv; mouse; ss.
XX	
OS	Mus sp.
XX	
PN	WC0925818-A1.
XX	
PD	27-MAY-1999.
XX	
PF	16-NOV-1998; 98WO-EP07313.
XX	
PR	17-NOV-1997; 97EP-0120096.
XX	
PA	(KUEE/) KUEER P.
XX	
PI	Borschert K, Kufer P, Lutterbuese R, Raum T, Zettl F;
XX	
DR	WPI; 1999-338004/28.
DR	P-PSDB; Y17958.
XX	

PI	Borschert K, Kuter P, Lutterbuese R, Raum T, Zetl F
XX	
XX	
DR	WPI: 1999-338004/28.
DR	P-PSDB: Y17958.
XX	
XX	

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QY	656	tggagatttatattgtctgcaagagtaacacattctccgtctacgtgtctgtctgcacaca	715
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ID	X86942		
XX	X86942	strand: DNA: 726 BP.	
AC	X86942:		
XX	24-SEP-1999	(first entry)	
DE	Antibody BIOC7 encoding DNA.		
XX	Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody;		
KW	diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy;		
KW	BIOC7; ds.		
XX	Homo sapiens.		
OS	EP934953-A2.		
PN	11-AUG-1999.		
XX	01-DEC-1998:	98EP-0122546.	
PD	03-DEC-1997:	97US-0067428.	
XX	(BOEF) BOEHRINGER MANNHEIM CORP.		
PA	Mahoney W, Sawyer JR, Winter GP:		
PI	WP1: 1999-432068/37.		
XX	P-PSDB: Y21884.		
DR	New anti-complex antibody useful for diagnosing prostate cancer		
XX	Disclosure; Page 28-30; 42pp: English.		
PS	The invention relates to an antibody that binds a complex between		
CC	prostate-specific antigen (PSA) and anti-chymotrypsin (ACT), and has an		
CC	affinity for the complex which is at least 10 fold higher than the		
CC	affinity for either PSA or ACT alone. The antibody is used in diagnostic		
CC	assays to detect PSA-ACT in serum samples from patients. The levels of		
CC	PSA-ACT complex increase in patients suffering from prostate cancer		
CC	compared to the levels in patients with benign or no growths in the		
CC	prostate. Therefore detection of PSA in complex with ACT is useful for		
CC	the early detection of prostate tumours, by distinguishing between benign		
CC	and malignant conditions of the prostate as well as for the management of		
CC	patients with prostate cancer, such as the disclosure of metastasis and		
CC	the monitoring of the PSA levels after treatment. The antibodies may		
CC	also be used in immunotherapy, affinity chromatography and isolation or		
CC	purification of PSA-ACT. Unlike prior art antibodies which bind to		
CC	PSA-ACT complexes but may also bind PSA or ACT alone, the present		
CC	antibody is specific for PSA-ACT alone. Diagnostic assays using the		
CC	antibodies are more accurate in diagnosing prostate cancer as they only		

CC detect the intact complex of PSA-AcT. Sequences Y21880-884 represent
CC specific examples of antibodies directed against PSA-AcT. The present
CC sequence represents the nucleotide sequence of antibody B10C7.
XX
SQ Sequence 726 BP; 167 A; 178 C; 217 G; 161 T; 3 other;

Query Match	57.3%;	Score 418;	DB 20;	length 726;
Best Local Similarity	75.3%;	Pred. NO. 6.4e-111;		
Matches 549;	Conservative	1;	Mismatches 167;	Indels 12;
				Gaps 2;

[illegible]

Search completed: February 17, 2001, 23:01:10
Job time: 16451 sec ;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 20:27:22 ; Search time 2148.34 Seconds

(without alignments)
1473.291 Million cell updates/sec

Title: US-09-297-181-1

Perfect score: 729

Sequence: 1 caggtgcagctgcagcagctc.....gcaccacgtggaatcaaa 729

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 12370408 seqs, 2170871038 residues

Total number of hits satisfying chosen parameters: 24740816

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Pending_Patents_NA.*

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Print. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	729	100.0	729	16	US-09-297-181-1
2	717.8	98.5	768	13	US-08-930-480-4
3	717.8	98.5	768	13	US-08-930-480A-4
4	716.2	98.2	749	13	US-08-983-035-16
5	716.2	98.2	1611	13	US-08-983-035-37
6	505	69.3	1135	16	US-09-203-958-2
7	464.8	63.8	819	55	US-09-523-095A-33
8	464.8	63.8	828	55	US-09-523-095A-31
9	460.8	63.2	747	16	US-09-297-181-3
10	460	63.1	741	55	US-09-523-095A-39
11	458.4	62.9	819	55	US-09-523-095A-29
12	458.4	62.9	828	55	US-09-523-095A-25
13	438	60.1	714	21	US-09-559-019-10
14	436.4	59.9	720	21	US-09-559-019-19
15	426.6	58.5	753	1	PCR-US00-19843-16
16	426.6	58.5	792	1	PCR-US00-19843-9
17	425.2	58.3	1679	17	US-09-364-088-15
18	425.2	58.3	1679	19	US-09-523-279-15
19	425.2	58.3	1679	55	US-09-188-082-15
20	418	57.3	726	16	US-09-202-000-13
21	418	57.3	726	16	US-09-202-000-15
22	409.4	56.2	830	17	US-09-358-371A-31
23	405.8	55.7	879	16	US-09-235-073-22
24	402.6	55.2	786	1	PCR-US00-19843-17
25	402.6	55.2	792	1	PCR-US00-19843-10
26	392	53.9	1047	22	US-09-646-028-35
27	392	53.8	1086	22	US-09-646-028-37
28	369.6	50.7	783	21	US-09-589-870-36
29	361.8	49.6	772	7	US-08-331-396-33
30	361.8	49.6	772	7	US-08-331-396A-33
31	361.8	49.6	772	7	US-08-331-396C-33
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33	361.8	49.6	772	7	US-08-331-397-33
34	361.8	49.6	772	7	US-08-331-398-33
35	361.8	49.6	772	11	US-08-759-804-33
36	361.8	49.6	772	16	US-09-227-653-33
37	358.2	49.1	771	19	US-09-526-728-1
38	358.2	49.1	780	19	US-09-526-728-3
39	356.8	48.3	1725	18	US-09-468-029-57
40	352.4	48.3	720	16	US-09-206-595-7
41	349.2	47.3	1668	18	US-09-468-029-59
42	349	47.9	738	7	US-08-331-396C-31
43	349	47.9	741	7	US-08-331-396D-31
44	349	47.9	741	7	US-08-331-396E-31
45	349	47.9	741	7	US-08-331-396A-31

ALIGNMENTS

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RESULT 1
US-09-297-181-1
; Sequence 1, Application US/09297181
; GENERAL INFORMATION:
; APPLICANT: Bracco, Laurent
; APPLICANT: Debussche, Laurent
; TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES
; FILE REFERENCE: ST96030-US
; CURRENT APPLICATION NUMBER: US/09/297,181
; CURRENT FILING DATE: 1999-04-26
; EARLIER APPLICATION NUMBER: PCT/FR97/01921
; EARLIER FILING DATE: 1997-10-27
; EARLIER APPLICATION NUMBER: FR96/13176
; EARLIER FILING DATE: 1996-10-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(729)
US-09-297-181-1

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Query Match      100.0%; Score 729; DB 16; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.8e-207;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 caggtgagctgcagcagctctggggcagagcttggaggtcaggggcctcaagttg 60
QY 61 tccgcagccttcctgcctcaacatcaagacacacatctgacgtgggagcagag 120
DB 61 tctctcagccttcctgcctcaacatcaagacacacatctgacgtgggagcagag 120
QY 121 cctgaacagggcctgagatgagatgagatgagatgagatgagatgagatgagat 180
DB 121 cctgaacagggcctgagatgagatgagatgagatgagatgagatgagatgagat 180
QY 181 gcccgaagttcagggcagggcagggcagggcagggcagggcagggcagggcaggg 240
DB 181 gcccgaagttcagggcagggcagggcagggcagggcagggcagggcagggcaggg 240
QY 241 ctgcagctcagcagcctgcagcctgcagcctgcagcctgcagcctgcagcctgcag 300
DB 241 ctgcagctcagcagcctgcagcctgcagcctgcagcctgcagcctgcagcctgcag 300
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DB 301 gatgcttgcagctatggggcagggcagggcagggcagggcagggcagggcagggc 360
QY 361 tcagggcagggcagggcagggcagggcagggcagggcagggcagggcagggcaggg 420
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QY 481 ttgatgtatggaagacatatgtatgtatgtatgtatgtatgtatgtatgtatgtat 540
DB 481 ttgatgtatggaagacatatgtatgtatgtatgtatgtatgtatgtatgtatgtat 540
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DB 541 aagcgcttaatactatctgtgtctaaactggaactggaactggaactggaactgga 600
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DB 601 agtggatcagggagagttcacaactaaatacaagagatggaggtggaggtggaggt 660

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QY 721 gaatacaaa 729
DB 721 gaatacaaa 729

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RESULT 2
US-08-930-480-4
; Sequence 4, Application US/08930480
; GENERAL INFORMATION:
; APPLICANT: BRACCO, Laurent
; APPLICANT: SCHNEIGHOFER, Fabien
; APPLICANT: TOCQUE, Bruno
; TITLE OF INVENTION: CONDITIONAL EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,480
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/03841
; FILING DATE: 31-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR96/00477
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fehner Esq., Paul F.
; REGISTRATION NUMBER: 35,135
; REFERENCE/DOCKET NUMBER: ST95021-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-930-480-4

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Query Match      98.5%; Score 717.8; DB 13; Length 768;
Best Local Similarity 99.0%; Pred. No. 4.2e-204;
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QY 61 tccctgacagctctggtctcaacatcaagacacacacacacacacacacacacacac 120
DB 88 TCTGTGACAGCTCTGTGCTTCAACATTAAGACTATATGCACTGGGTGAAGCAGAGG 147
QY 121 cctgaacagggcctgagaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtg 180
DB 148 CCGAACAGGGCCTGAGAGTGGATTGATGATGATGATGATGATGATGATGATGATGAT 207

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Oy	181	gccccgaagctcccaaggagcaagccacatctgacctgcacacacatccctcaataagccttac	240
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Oy	241	ctgcagcctcagcagcctctgcactctgaagacacactgcgctctatacttattgtaattttacg	300
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Oy	301	gatgccttggactattgaggcccaaggagccacggtcacagctctcctcaagtgtgagggcgt	360
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Oy	421	acttgctcggttaccattgagcaacccagccctccactctcttcgaagtcaagtccagcctc	480
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Oy	541	aagcgcccaactatctggtgtctcaaacctgagcctctgagcctccaggttaccgctc	600
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Oy	601	agtgatcaaggagacagatcttcacactgaaatacaacagagtgtagagcttggaattgga	660
Db	628	agtgatcaaggagacagatcttcacactgaaatacaacagagtgtagagcttggaattgga	687
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: RESULT 3
: US-08-930-480A-4
: Sequence 4, Application US/08930480A
: GENERAL INFORMATION:
: APPLICANT: BRACCO, Laurent
: APPLICANT: SCHWEIGHOFER, Fabien
: APPLICANT: TOCOUE, Bruno
: TITLE OF INVENTION: CONDITIONAL EXPRESSION SYSTEM
: FILE REFERENCE: ST95021-US
: CURRENT APPLICATION NUMBER: US/08/930,480A
: CURRENT FILING DATE: 1998-01-21
: PRIOR APPLICATION NUMBER: PCT/FR96/00477
: PRIOR FILING DATE: 1996-03-29
: PRIOR APPLICATION NUMBER: FR95/03841
: PRIOR FILING DATE: 1995-03-31
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 768
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Scrv Against
: OTHER INFORMATION: p53
: US-08-930-480A-4

Query Match      98.5%; Score 717.8; DB 13; Length 768;
Best Local Similarity 99.0%; Pred. No. 4,2e-204;
Matches 722; Conservative 0; Mismatches 7; Indels 0; Gaps 0

```

QY	1	caaggtgcagcgcagcagcaatcctcgggagcagaagctcttgaggttcaaggagccatgaataatg	60
DB	28	caaggtgcagcgcgcagcagcagctcctgggagcagaagctctgaaggtcgaaggccctcaagtcagt	87
QY	61	tctctgcacagcttctcgtctcctaacaattaaagaactataatgcactcgtgtgtaagcagag	120
DB	88	tctctgcacagcttctcgtctcctaacaattaaagaactataatgcactcgtgtgtaagcagag	147
QY	121	cctgcagacgggcctcggagtgagttgagttgatactctgcagaatggtgtgatactgaaat	180
DB	148	cctgcagacgggcctcggagtgagttgagttgatactctgcagaatggtgtgatactgaaat	207
QY	181	gcccccgaagcttcacaggagggaagggacactatgtacctgcagacaacatccctcaatacagccctac	240
DB	208	gcccccgaagcttcacaggagggaagggacactatgtacctgcagacaacatccctcaatacagccctac	267
QY	241	ctgcagacctaagcagcctctgcagctctctgaagagacactcgcgtctataatgtgtaattttaaagg	300
DB	268	ctgcagacctaagcagcctctgcagcctctctgaagagacactcgcgtctataatgtgtaattttaaagg	327
QY	301	gattgcttttgacattatggggcccaaggagacacagcgttcacacgtctcctcaagtctgagagcgt	360
DB	328	gattgcttttgacattatggggcccaaggagacacagcgttcacacgtctcctcaagtctgagagcgt	387
QY	361	tcaaggccggagagtggtctcctcgcgcgtgcggagatccgagatttttgatagaccacaactccactc	420
DB	388	tcaaggccggagagtggtctcctcgcgcgtgcggagatccgagatttttgatagaccacaactccactc	447
QY	421	actttgtcgtgttaccatctgagacaacacagcctccactcctcttgcaagttcagagacgtc	480
DB	448	actttgtcgtgttaccatctgagacaacacagcctccactcctcttgcaagttcagagacgtc	507
QY	481	ttggaatagtgatgtaagaagacatatctgaattggtgtgtacaagagccagccagctctca	540
DB	508	ttggaatagtgatgtaagaagacatatctgaattggtgtgtacaagagccagccagctctca	567
QY	541	aagcgcctcaactctatctcgtgtgtctaaactggaacctcgtgaggtcccttcagagttcaactcgc	600
DB	568	aagcgcctcaactctatctcgtgtgtgtctaaactggaacctcgtgaggtcccttcagagttcaactcgc	627
QY	601	agtgtatcagggagacagatattcacactgtaaatacaacagagtgtagaggtctgtagatttgga	660
DB	628	agtgtatcagggagacagatattcacactgtaaatacaacagagtgtagaggtctgtagatttgga	687
QY	661	gtttatattctcgtgcgaaggtacacatctcctcgtctcaagttcgtgtcgtgcagaccagctg	720
DB	688	gtttatattctcgtgcgaaggtacacatctcctcgtctcaagttcgtgtcgtgcagaccagctg	747
QY	721	gaatatcaaa 729	
DB	748	gaatatcaaa 756	

RESULT 4
US-08-983-035-46
Sequence 46, Application US/08983035
GENERAL INFORMATION:
APPLICANT: BRACCO, Latent
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
TITLE OF INVENTION: US\$ THERBOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

COMPUTER READABLE FORM:
- MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```


Query Match	63.28;	Score 460.8;	DB 16;	Length 747;
Best Local Similarity	79.28;	Pred. No. 4.6e-127;		
Matches 594;	Conservative 0;	Mismatches 132;	Indels 24;	Gaps 3

Accession	Sequence	Position
D6	gtccctgatcgcttcaacaggcagcggatcgctcgggacacagattcaactctccaccatccacgaagcagt	660
Qy	gtggagagctaaagaaattggggagattatattttgcgggaaggtacacattcttcgcgtcag	699
D6	gtgcagcgctgaagaccgcgcgcatattatattactgtcgaagaa---tctataatctcacgcagc	717
Qy	ttcgtgtctgtgcaccaaagctggaaattcaaa	729
D6	tttcgcgcgggacacaaagcttggaaattcaaa	747

Query Match	63.1%;	Score 460;	DB 55;	Length 741;
Best Local Similarity	77.7%;	Pred. NO. 8e-127;		
Matches 569;	Conservative	0;	Mismatches 160;	Indels 3; Gaps 1;

OY	1	caagtcgacgacgacgacgtctcgggacgaagcttctgtggtgctcaggcgccctgaatcgaattg	60
Db	4	caagtcgaactccaacgactcctcgaccctggaaactggtlaaagcctgggtcttcagtgaaatg	63
OY	61	tcctgcacagcttctctgcttccaacattaaagactactatatactgactctgtgtgaagcagaag	120
Db	64	tcctgcagaaggtctctgtgataacactctgctaaacattgatttaactctgtgtgtgaagcagaag	123
OY	121	ccctgaacaggtgcccgagctgtgattctgtatgtgatacttcgaagaatgtgtgatactgataat	180
Db	124	ccaaagccaggtgacctctgtgagatgtgataattatcttcaacaatgtgtgtactaaatg	183
OY	181	ggcccgaaagttccagggccagaagccacactatgctcagaacacatcctccaatcagacctac	240
Db	184	aatgagaaagttccaagggccaagggccacacctctgaacttcagacaacaatcctccacacagcctac	243
OY	241	ctgcagactcagaaagcctggacatctgagagacactgtcgcttataattgtaaatttttaacg	299
Db	244	atgagacactccaacagcctgtgcctctcgtagagactctggtctataactctgtcagaaggggt	303
OY	300	ggatgcttcttgagactcttttgagccagaagggaacacaggttaacacctctcctaagcttgaggc	357
Db	304	tactatacttcgacgacgtcggtggccaaaggaacacacctccacaaagctctctcaagcttggtgt	363
OY	358	ggctcagaagcagaaagctgtgctctctgtgcgtgtgcagatcggatgtttttgatgacccaactcca	417
Db	364	ggttcgggtgtgtgtgtcttcgggtgtgtgtgtgcgagatcggatgtgtgtgatgacccaagtcca	423
OY	418	ctcaactctgtgttaccatttggacaaacccgctccatctcttcgaaagttaagtctagagc	477
Db	424	ctctccccgctctgtcactctctgtgagatacaagccctccatctcttcgacgataaagctcagagc	483


```
OY 181 gccccgaagttccagggcgaagccactatgactgacagacacatccctccatacagctac 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 aatgagaagtccaagggcgaagccacacagctactcagaataatccctccagcgagctac 306
OY 241 ctgcagctacagcagctgacatctgagacacatgcccgtatattatatttttcagg- 239
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 atggaactcagcagcctgctcctctgagactctgctactactactgctgaagagggt 366
OY 300 --gagatcttgtagctatggggcgaagcagcagcagctccctccctcagttgaggc 357
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 tactaatgtaacgacgacctggggcgaagcaccacccctccctccctcagttggtc 426
OY 358 ggttcagcggcaggtggtcctcctggcggcggcggatctgatttgaatgaacccaatcca 417
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 ggttcgggggtggtggttcgggtggtggtggtggtggtggtggtggtggtggtggt 486
OY 418 ctcaacttgcgttccatctgacacacacacacacacacacacacacacacacacacac 477
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 ctctccctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 546
OY 478 ctcttgatagtgatgaaagacatatttgattggttttaagaggccagcgagctct 537
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 547 ctctacacagtaagaaacacacacacacacacacacacacacacacacacacacacac 606
OY 538 ccaagcgcctactatctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 597
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 607 ccaagcctcctgctcctcaaaagttccaaacggatttctgggggtccacagcaggttcagt 666
OY 598 ggcagtgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 657
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 667 ggcagtgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 726
OY 658 ggcagtgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 717
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 727 ggcagtgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 786
OY 718 ctggaatacaaa 729
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 787 ctggaatacaaa 798
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-559-019-30
; Sequence 30, Application US/09559019
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Wille, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: Sequence Listings 1-34 for 381-71
; CURRENT APPLICATION NUMBER: US/09/559,019
; CURRENT FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Mouse
US-09-559-019-30
```

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Query Match          60.1%; Score 438; DB 21; Length 714;
Best Local Similarity 77.3%; Pred. No. 3,1e-120;
Matches 566; Conservative 0; Mismatches 145; Indels 21; Gaps 2;
```

OY 1 caggtgcagctcagcagcagctggtggcagagcctgtgagtgacaggggctcagtcagttg 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 caggtcagctcagcagcagctggtggcagagcctgtgagtgacaggggctcagtcagttg 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 tctgtcagcagctctggtctcacaataaagactactatgacagcgggtgaagcagagg 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 tctgtcagcagctctggtctcacaataaagactactatgacagcgggtgaagcagagg 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 121 cctgacaagcgtctggtgagtgatgagtgatctctcagtaagtgtgatactgataat 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 121 cctgacaagcgtctggtgagtgatgagtgatctctcagtaagtgtgatactgataat 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 181 gccccgaagttccagggcgaagccactatgactgacagacacatccctccatacagctac 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 gccccgaagttccagggcgaagccacacagctactcagaataatccctccagcgagctac 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 241 ctgcagctacagcagctgacatctgagacacatgcccgtatattatatttttcagg 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ctgcagctacagcagctgacatctgagacacatgcccgtatattatatttttcagg 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 301 gatgctttgga---ctatggggccaaggggacacagcagtcacgctcctcccaagttgaggc 357
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 ggtgactacgaagcgtactcagcagcagggacacagcagcagcagcagcagcagcagcagc 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 358 ggttcagcggcaggtggtcctcctggcggcggcggatctgagtgatttgaatgaacccaatcca 417
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 ggttcagcggcaggtggtcctcctggcggcggatctgagtgatttgaatgaacccaatcca 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 418 ctcaacttgcgttccatctgacacacacacacacacacacacacacacacacacacac 477
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 gcaatcagtgctgcatctccagggaggaaggtccacacacacacacacacacacacacac 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 478 ctcttgatagtgatgaaagacatatttgattggtttgaacagggccagcgagctct 537
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 gta-----agttacatgacactggttcacagcagaaagcagcgagcactct 522
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 538 ccaagcgcctactatctatctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 597
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 523 ccaaacctctgatttgaacacatccacacacacacacacacacacacacacacacacacac 582
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 598 ggcagtgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 657
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 583 ggcagtgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 642
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 658 ggcagtgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 717
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 643 ggcagtgatgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 702
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 718 ctggaatacaaa 729
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 703 ctggaatacaaa 714
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 14
US-09-559-019-29
; Sequence 29, Application US/09559019
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Wille, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: Sequence Listings 1-34 for 381-71
; CURRENT APPLICATION NUMBER: US/09/559,019
; CURRENT FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Mouse
US-09-559-019-29
```

Query Match 59.9%; Score 436.4; DB 21; Length 720;
Best Local Similarity 77.2%; Pred. No. 9,3e-120;
Matches 565; Conservative 0; Mismatches 146; Indels 21; Gaps 2;

OY 1 caggtgcagctcagcagcagctggtggcagagcctgtgagtgacaggggctcagtcagttg 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 caggtcagctcagcagcagctggtggcagagcctgtgagtgacaggggctcagtcagttg 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 tctgtcagcagctctggtctcacaataaagactactatgacagcgggtgaagcagagg 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||


```

Db 61 tccctgacaaactctgctcacaatlaaagaacttctatatgcatggtgtgaagcagaag 120
QY 121 cctgaacagagcctgagtgatgtgattgattcctagaatgtgtactaatat 180
Db 121 cctgaacagagcctgagtgatgtgattgattcctagaatgtgtactaatat 180
QY 181 gccccgaagttccagggcagaagccacatgacgtcagacatccctcaacacagctac 240
Db 181 gccccgaagttccagggcagaagccacatgacgtcagacatccctcaacacagctac 240
QY 241 ctgcagctcagcagcctgagctatgtgaagacacgtccgtctattatgttaatttttaagg 300
Db 241 ctgcagctcagcagcctgagctatgtgaagacacgtccgtctattatgttaatttttaagg 300
QY 301 gatgcttga---ctattgggccaaggagacacagctccctcctcaagtgagagc 357
Db 301 gaggactacgaagcctcagctgagggccaaggagacacagctccctcctcaagtgagagc 360
QY 358 ggttcagagcgagagtgctgctgagcggtgagcagatgttttgaatgacccaactcca 417
Db 361 ggttcagagcgagagtgctgctgagcggtgagcagatgttttgaatgacccaactcca 420
QY 418 ctactctgtcggttaccatgtgacacacagcctccctcttgcaagatgaatcagagc 477
Db 421 gcaatcatgtctgcatctccagggaggaagtcacacacacacgtgcagcagcctcaagt 480
QY 478 ctcttgatgtgatgaaagacatattgattgtgtgtacagaagcgccagcagctc 537
Db 481 gta-----agttacatgcatgtgttccagcagagaagcagcagcacttc 552
QY 538 ccaagcgcttaactatctgtgtctaaactggaactgtgagtcctcctgaaggttcaact 557
Db 523 cccaactctggtattatagcacatccacacactgctgtcgtgagtcctcgtcgttcaagt 582
QY 598 ggaagtgatcagagcagattcacaactgaataacacagagtgagtgagtgagtttg 657
Db 583 ggaagtgatcagagcagattcacaactgaataacacagagtgagtgagtgagtttg 642
QY 658 ggaagtgatcagagcagattcacaactgaataacacagagtgagtgagtgagtttg 717
Db 643 ggaagtgatcagagcagattcacaactgaataacacagagtgagtgagtgagtttg 702
QY 718 ctggaatacaaa 729
Db 703 ctggaatacaaa 714

RESULT 15
PCT-US00-19843-16
; Sequence 16, Application PC/TUS0019843
; GENERAL INFORMATION:
; APPLICANT: Herr, John C.
; APPLICANT: Norton, Elizabeth J.
; APPLICANT: Deikman, Alan B.
; TITLE OF INVENTION: Recombinant Antibody Directed Against Human Sperm
; FILE REFERENCE: 00415-02
; CURRENT APPLICATION NUMBER: PCT/US00/19843
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/145,512
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentlin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Mus musculus
; PCT-US00-19843-16

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Query Match 58.5%; Score 426.6; DB 1; Length 753;
Best Local Similarity 74.8%; Ptd. No. 8.3e-117;
Matches 550; Conservative 0; Mismatches 179; Indels 6; Gaps 1;

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QY 1 caaggtcagcctgagcagctctgggagagctgtgtgaagtcaggggcctcagtcaggttg 60
Db 7 caaggtcagcctgagcagcagctctgggagagctgtgtgaagtcaggggcctcagtcaggttg 66
QY 61 tccctgacaaactctgctcacaatlaaagaacttctatatgcatggtgtgaagcagaag 120
Db 67 tccctgacaaactctgctcacaatlaaagaacttctatatgcatggtgtgaagcagaag 126
QY 121 cctgaacagagcctgagtgatgtgattgattcctagaatgtgtactaatat 180
Db 127 cctgaacagagcctgagtgatgtgattgattcctagaatgtgtactaatat 186
QY 181 gccccgaagttccagggcagaagccacatgacgtcagacatccctcaacacagctac 240
Db 187 gatgtgaagttccagggcagaagccacatgacgtcagacatccctcaacacagctac 246
QY 241 ctgcagctcagcagcctgagctatgtgaagacacgtccgtctattatgtt-----aatttt 294
Db 247 atacaactcagcagcctgagctatgtgaagacacgtccgtctattatgtt-----aatttt 306
QY 295 taaggagatgtgtgactattggggccaaggagacacagcgtccctcctcaagtgaga 354
Db 307 tatgtgtcccttctgttactgagggccaaggagacacagcgtccctcctcaagtgaga 366
QY 355 ggcgtgtcagcgagagtgctgctgagcggtgagcagatgttttgaatgacccaact 414
Db 367 ggcgtgtcagcgagagtgctgctgagcggtgagcagatgttttgaatgacccaact 425
QY 415 ccaactcatttgcgttccatgtgacacacagcctccatctcttgcagatgaatcag 474
Db 427 ccaactcatttgcgttccatgtgacacacagcctccatctcttgcagatgaatcag 486
QY 475 agccttggatgtgatgaaagacatattggaattgtgtgttacaaggcgccagcgag 534
Db 487 agccttggatgtgatgaaagacatattggaattgtgtgttacaaggcgccagcgag 546
QY 535 tctcacaagcgccttaactatctgtgtctaaactggaactgtgagtcctcctgaacaggttc 594
Db 547 tctcacaagcgccttaactatctgtgtctaaactggaactgtgagtcctcctgaacaggttc 606
QY 595 actgagcagtgatcagagcagattcacaactgaataacacagagtgagtgagtgagat 654
Db 607 actgagcagtgatcagagcagattcacaactgaataacacagagtgagtgagtgagat 666
QY 655 ttggagatttattgtcgtgagaggttacacattcccgctcaagctgtgctgagcacc 714
Db 667 ctggagatttattgtcgtgagaggttacacattcccgctcaagctgtgctgagcacc 726
QY 715 aagctggaatacaaa 729
Db 727 aagctggaatacaaa 741

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Search completed: February 18, 2001, 01:29:16
Job time: 18114 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2001, 13:14:09 ; Search time 83.91 seconds
(without alignments)
1400.141 Million cell updates/sec

Title: US-09-297-181-1

Perfect score: 729

Sequence: 1 caggtcagctgcagcagtc.....gcacacagctggaatcaaa 729

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued_Patents_NA:*
2: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCRTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Dackfilest1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	59.7	907	US-09-184-658-9	Sequence 9, Appl
2	432.2	59.3	810	US-08-652-507-1	Sequence 1, Appl
3	425.2	58.3	1679	US-08-661-052-15	Sequence 15, Appl
4	407.4	55.9	1095	US-08-875-811-52	Sequence 52, Appl
5	407.4	55.9	1098	US-08-875-811-54	Sequence 54, Appl
6	361.8	49.6	772	US-08-331-398A-33	Sequence 33, Appl
7	361.8	49.6	772	US-08-331-397B-33	Sequence 33, Appl
8	361.8	49.6	772	US-08-759-804A-33	Sequence 33, Appl
9	352.4	48.3	720	US-09-296-595-7	Sequence 7, Appl
10	352.4	48.3	720	US-09-296-595-7	Sequence 7, Appl
11	349.2	47.9	1797	US-08-463-163-2	Sequence 31, Appl
12	349	47.9	738	US-08-331-398A-31	Sequence 31, Appl
13	349	47.9	738	US-08-331-397B-31	Sequence 31, Appl
14	349	47.9	738	US-08-759-804A-31	Sequence 31, Appl
15	347.6	47.7	719	US-08-279-772A-7	Sequence 7, Appl
16	347.6	47.7	720	US-08-902-486-10	Sequence 10, Appl
17	339.8	46.6	756	US-08-797-689-17	Sequence 17, Appl
18	339	45.1	814	US-08-752-844-65	Sequence 65, Appl
19	332	44.2	726	US-08-553-497A-25	Sequence 25, Appl
20	318.2	43.6	2012	US-08-235-838-15	Sequence 15, Appl
21	318.2	43.6	2012	US-08-465-473B-15	Sequence 15, Appl
22	315.6	43.3	748	US-08-235-838-10	Sequence 10, Appl
23	315.6	43.3	748	US-08-465-473B-10	Sequence 10, Appl
24	312.2	42.8	831	US-08-403-853-17	Sequence 17, Appl
25	308.2	42.3	732	US-08-553-497A-19	Sequence 19, Appl
26	306.6	42.1	1065	US-08-875-811-56	Sequence 56, Appl
27	305.6	41.9	336	US-08-678-194-5	Sequence 5, Appl
28	305.4	41.9	354	US-08-767-128-21	Sequence 21, Appl

29	305.2	41.9	924	US-08-860-174A-9	Sequence 9, Appl
30	305	41.8	726	US-08-553-497A-27	Sequence 27, Appl
31	302.4	41.5	336	US-09-184-658-11	Sequence 11, Appl
32	300.2	41.2	732	US-08-553-497A-21	Sequence 21, Appl
33	299.4	41.0	780	US-08-447-402-6	Sequence 6, Appl
34	298.8	41.0	797	US-08-894-922A-13	Sequence 13, Appl
35	297.6	40.8	2165	US-08-263-911-6	Sequence 6, Appl
36	297.6	40.8	2165	US-08-263-911-6	Sequence 6, Appl
37	297.2	40.8	891	US-08-894-922A-9	Sequence 9, Appl
38	290.6	39.9	738	US-08-553-497A-23	Sequence 23, Appl
39	288	39.5	1460	US-08-392-388A-18	Sequence 18, Appl
40	288	39.5	1460	US-09-166-750-18	Sequence 18, Appl
41	288	39.5	1460	US-09-166-093-18	Sequence 18, Appl
42	288	39.5	1460	US-09-172-019-18	Sequence 18, Appl
43	288	39.5	1460	US-09-166-094-18	Sequence 18, Appl
44	285	39.1	712	PCT-US92-08257-8	Sequence 8, Appl
45	284	39.0	858	US-08-428-257A-71	Sequence 71, Appl

ALIGNMENTS

```

RESULT 1
US-09-184-658-9      : Sequence 9, Application US/09184658
: Patent No. 6030792
: GENERAL INFORMATION:
: APPLICANT: Otterness, Ivan G.
: APPLICANT: Mezes, Peter S.
: APPLICANT: Downs, James T.
: APPLICANT: Johnson, Kimberly S.
: TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
: TITLE OF INVENTION: Biological Media
: FILE REFERENCE: PC9946-A
: CURRENT APPLICATION NUMBER: US/09/184,658
: CURRENT FILING DATE: 1998-11-02
: EARLIER APPLICATION NUMBER: 60/065,423
: EARLIER FILING DATE: 1997-11-13
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: Patentia Ver. 2.0
: SEQ ID NO 9
: LENGTH: 907
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
: NAME/KEY: sig_peptide
: LOCATION: (29)..(94)
: OTHER INFORMATION: Engineered signal peptide in pCANTAB6; initiator
: OTHER INFORMATION: methionine is coded for most likely by gtc codon.
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: (95)..(895)
: OTHER INFORMATION: Coding sequence for genetically engineered single
: OTHER INFORMATION: chain antibody - 5109 VH - VL.
US-09-184-658-9

Query Match          59.7%; Score 435; DB 3; Length 907;
Best Local Similarity 75.6%; Pred. No. 5e-119;
Matches 553; Conservative 0; Mismatches 175; Indels 3; Gaps 1;

QY 2 aggtcagctgcagcagctggtgagcagcgtgtgaggtcagggcctcagtaagtgt 61
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DB 36 aagtcagctgtgtgagcgtgtgagcagcgtgtgaggtcagcctggaactct 155
   |||||

QY 62 cctgcagcgttcgtgctcaacataaagcactatcagcactggtgagcagagc 121
   |||||
DB 156 cctgcagcgttcgtgctcaacataaagcactatcagcactggtgagcagc 215
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QY 122 ctgacacagggcctgagagtgatgtgatgtgaccccgagaatggtgatactatg 181

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Db 216 cagacagaagcgtgagtggtgcaaccatattagtagtggtgtctacattatg 275
QY 182 ccccgagatccagcagaagccacatagctgacagacatctccatatacagctacc 241
Db 276 cagacagtgtagaagggccgattccacattccagagaacatggcacaacacccctatc 335
QY 242 tgcagctcagcagcctgagcatctgagagacatgctgctatattatgtaattttacgggg 301
Db 336 tgcgaatgacagcagcgaagtcgtggagcctcagcagcagctgattactgtgtaagagata 395
QY 302 atgcttgactcttggtggcagaagccacagctcaccgtctctcagtggtggaggggtt 361
Db 396 gtaattacgcctgcgtgggcaagggcgctgctcactgctcagtggtggagggcggtt 455
QY 362 cagcgagagtggtcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 418
Db 456 cagcgagagtggtcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 515
QY 419 tcacttgctggttaccatgagcaacacagcctcactctctgcaagtcagagtcagagcc 478
Db 516 tcacttgctggttaccatgagcaacacagcctcactctctgcaagtcagagtcagagcc 575
QY 479 tcttgatagtgtagtgaagacatattgtaattggtttacagagggccagagctc 538
Db 576 tcttgatagtgtagtgaagacatattgtaattggtttacagagggccagagctc 635
QY 539 caaagcgctaatctatctggtgtctaaactgagctgagtcctctgcaaggttaccgt 598
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Db 696 gcaatgagtcagaggaagatttcaacatgaaatcaacagagtgagagtggtgagattgg 755
QY 659 gagttattatattgctggaaggaacatctcctcgtcactggttgcgtgagccaagc 718
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QY 719 tgaagaatcaa 729
Db 816 tgaagctgaa 826

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TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 810 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-652-507-1

Query Match 59.3%; Score 432.2; DB 2; Length 810;
Best Local Similarity 76.7%; Pred. No. 3.2e-118;
Matches 568; Conservative 0; Mismatches 143; Indels 30; Gaps 2;

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QY 61 tcttcacagcttctggtcctcaacttaagactactatgctggtggtggtggtggtggtggtggt 120
Db 139 tcttcacagcttctggtcctcaacttaagactactatgctggtggtggtggtggtggtggt 198
QY 121 cctgacagaggtcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 180
Db 199 CCTGAACAGGCGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 258
QY 181 gccccgaagttccagaggaagccactatgactgagagacactctccatcaacacac 240
Db 259 GCCCGGAATCTCCAGGCGAGGCGCACTTTACTACAGACACTCTCCAGACACACTTAC 318
QY 241 cgtcagctcagagagctgcatctgagacactgagcagctgctatattgtaatt----- 291
Db 319 CTGCACTCAGCAGCCTGATCATCTGAGACACTGCCGCTATATTGTAATGAGGAGCT 378
QY 292 -----tttcagagagcttctgactattggtggcagaaggaagccagcgtcactcctca 348
Db 379 CCGACTGGGCGCTACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 438
QY 349 ggtgagagcgttcaagggagaggtggtcgtggtggtggtggtggtggtggtggtggtggt 408
Db 439 GGTGAGAGCGGTTCAAGCGGAGGAGTGGCTGTGGGCTGGCGGATCGAAGAAATGCTCTCAC 498
QY 409 caaatccactcacttctggttaccattgagacaacagccctccatctctgcaagta 468
Db 499 CAGTCTCCAGCATATGCTGTCATCTCCAGGAGGAGAGAGTACCATTAACCTCAGTGGC 558
QY 469 agtcagagcctctgtagatgtagtgaagacatatltgaattggttgttaccagagcca 528
Db 559 AGCTCAAGTGA-----AGTTCATGCACTGCTGCTCAGCAGAACCA 600
QY 529 ggtcagcttccaaagcgctaatctatctggttcaactgagctcgtggtggtcctcagc 588
Db 601 GGCACCTTCCCAAACTGTGATTTATGACATCAATCAACCTGGCTTTGGAGTCCCTCTCT 660
QY 589 agttcactgagcagtgtagtcaaggaacagattcacaactgaaatacaadaggttgaagct 648
Db 661 CCCTTCAGTGCACAGTGTGATCTGGGACCTTACTCTTCACATATGAGCGAATGAGGCT 720
QY 649 gaggaatttggagttattatattgctggaaggttacacatctcgcgtcagcttgcgtggt 708
Db 721 GAAATGCTGCGCATTATTATAGCGCAGGAAGAGTATGATCCCACTCAGCGTGGTCT 780
QY 709 ggcaccaagctggaatacaa 729
Db 781 GGCACCAAGCTGAGACTGAAA 801

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RESULT 3
US-08-661-052-15
; Sequence 15, Application US/08661052

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RESULT 4
 US-08-875-811-52
 Sequence 52, Application US/08875811
 Patent No. 6045793
 GENERAL INFORMATION:
 APPLICANT: *Hybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Luis
 APPLICANT: Wlodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: 2100 Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Fairs, Susan K.
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:


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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-1261400S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..772
OTHER INFORMATION: /note="Single-chain antibody fusion
OTHER INFORMATION: protein of B3 monoclonal antibody
OTHER INFORMATION: Variable Heavy chain (V-H) and Variable
OTHER INFORMATION: Light chain (V-L) Fv region joined by a
OTHER INFORMATION: (Gly-4Ser)-3 peptide linker"
FEATURE:
NAME/KEY: CDS
LOCATION: 27..770
US-08-759-804A-33

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Query Match          49.6%; Score 361.8; DB 2; Length 772;
Best Local Similarity 69.3%; Pred. No. 1.7e-97;
Matches 511; Conservative 0; Mismatches 217; Indels 9; Gaps 1;

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OY 2 agtgaagctgcagcagctgctggcagagctgtgtgaggtcagcctcaagtgt 61
DB 31 atgtgaagctgctgagctgctggcagagctgtgtgaggtcagcctcaagtgt 90
OY 62 cctgcagcttcctgctcctcaacattaaagactatatactgctggtgaagcagagc 121
DB 91 cctgtcgaacctgtgatttcttcttcttcttcttcttcttcttcttcttcttctt 150
OY 122 ctgaacagagcctgagctgagctgagctgagctgagctgagctgagctgagctgag 181
DB 151 cagagaagagctgagctgagctgagctgagctgagctgagctgagctgagctgag 210
OY 182 ccccgaaagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 241
DB 211 cagacactgtgaaagcctgcttccatcttccatcttccatcttccatcttccatctt 270
OY 242 tgcagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 292
DB 271 tgcgaatgagcctgtgaaatctgagagacacacacacacacacacacacacacacac 330
OY 293 tttaagcagctgcttgcagcttgcagcttgcagcttgcagcttgcagcttgcagcttgc 352
DB 331 cctggcagcagcctgtgttgccttgccttgccttgccttgccttgccttgccttgccttgc 390

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OY 353 gaagcagcttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 412
DB 391 gagcgcagctccgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 450
OY 413 cctcactccttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 472
DB 451 ctccattgattgattgattgattgattgattgattgattgattgattgattgattgattgattgatt 510
OY 473 agagccttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 532
DB 511 agatcattgattgattgattgattgattgattgattgattgattgattgattgattgattgattgatt 570
OY 533 agctccaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 592
DB 571 agctccaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 630
OY 593 tcactgagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 652
DB 631 tcagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 690
OY 653 attgagcttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgc 712
DB 691 actgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 750
OY 713 ccaagctggaatcaaa 729
DB 751 caaagctggaatcaaa 767

RESULT 9
US-08-800-198-7
Sequence 7, Application US/08800198
Patent No. 594,2602
GENERAL INFORMATION:
APPLICANT: WELLS, WINFRIED S.
APPLICANT: SCHMIDT, MATTHIAS
APPLICANT: VAKALOPOULOU, EVANGELIA
APPLICANT: SCHNEIDER, DOUGLAS
TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MILDEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,198
FILING DATE: 13-FEB-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: SCH 1576
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO

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	Query Match	Similarity	47.99	Score 349.2	DB 1	Length 1797
	Best Local	Similarity	65.06	Pred. No. 1.2e-93		
	Matches	Conservative	0	Mismatches 208	Indels 18	Gaps
QY	1	cagtgccagctcgcagcagctcctcgggacagagcttgagtgtaaggagcctcagtaagt	60			
Db	4	CAGGTCCAGCTGCAGCACTGTGGGGCTGCACTGGCAAAACCTGGGGCTCAGTGAAGTG	63			
QY	61	tccttcgcaagcttctcgtgcttcaaatcaatcaactacatatagcactcgtgtgtagcagaag	120			
Db	64	TCCTTCAAGGCTTCGGCTGCTACCTTTATAGCTACAGAGATGACCTGGTTAAACAAAGG	123			
QY	121	cctgacagagcgccttgagtgagcttgatgagatgcatcctgagaaagtgtgatactgaaat	180			
Db	124	CCTGCACAGGGCTCTGGAAATGGAATTGATATATTATACCTACCACTGGGTATATCAAGATAC	183			
QY	181	gcccccgaattccagagcgaagcccaactatgacttcgagacacacatccctccaatcacgcttac	240			

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Dbb      184 AATGAGAAATTCAAGACGAACAAGGCCACTTGTACCTGCAGAACAAATCCTCCACAGACGGTTAC   2433  
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QY       241 ctgcagcgcaggcaagctgtgacatctgaagacaactggccglctaattatigtaatltaaagg    3009  
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db        244 ATGCACATCGAAGCACCATTCGACATTTTGAGAAGACTTCGCAAGCTTAATACTCCAMAAGAGGGGG     3033  
  
QY       301 gatgccittgaccttttggcgccaagygaaaccaagtgaccgcltcctcctaagtltgaagcggt   3609  
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db        304 GGGGTCCTTAGCTCTCTGGGGCCAAGGAACCACCTCCACAGCTCTCTCCGAGAGCGGTGGC         3633  
  
QY       361 tcagcgcgagaagtgtgcctgtgcgftggcggaatcgatgtltagtatgaccsaactccactc           4209  
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db        364 TCGGGCCGGTGGCCGCTCGGGTGGCGGGCGGCGCTCTCAATTTGTTCTCACCCACGTCTCCAGCA   4233  
  
QY       421 acttgttgagttaccatitggacaacaccagccctcatactcttgcaagtlcaagtcagagctc       4809  
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db        424 ATCATGTCGTGATCTCCAGGGGGAAGAAGTCAACCATTAACCTGCAGTGCACGTCAAGATATA   4833  
  
QY       481 ttgatatagtatgaaaagaacatatattgaattgttgtttaaacagagcgcaagcccagcttcaa   5409  
          -----AGTTACATCATCACTGGTTCCAGCAAAGACGACGCACTTCCC             5255  
Db        484 -----AGTTACATCATCACTGGTTCCAGCAAAGACGACGCACTTCCC             5255  
  
QY       541 aaagccccaatctactctgygtfctcaaacigtgactctgagtcctctgaacagttcacatggc     6009  
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db        526 AAACCTCGGATTTTACCCACATCCACACCTGGCTTCTGAGTCCCTGCTCCTTCAGTGGC       5555  
  
QY       601 agtgcatacgggaacagaatttcacacgttcaaaaaacacacagagltggagctgtgagatttggaa   6609  
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db        586 AGTGAATCTGGGACCTCTTACTCTCTCCATCAATGACCCGANVGAGGGGTGAAGATGCTGCC       6455  
  
QY       661 gttattattgtcgtcaaggtataacatltccgcgtcaagtcagttggtgtgacccaagctg       7209  
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QY       721 gaatacaa 728  
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Db        706 GAGCTCAA 713
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RESULT 12
US-08-331-398A-31 :
Sequence 31 Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pat. Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: And Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:

OY	122	ctaaccaaggccctggagatggattgagatgagtcctccgaagaatgagatctatc	181
OY	122	ctaaccaaggccctggagatggattgagatgagtcctccgaagaatgagatctatc	181
DB	122	CGGGCAAGGGCCCTGGAGTGGGTCCGATCATTAATTAATGATGATGATGATTCGGCCCTTAAT	181
OY	182	cccccaagttcccaaggccaaggccactatgactgtgacacacacccccaataacagctacc	241
DB	182	CAGACACTGTAAAGGGCGGTTCAACACTCTAGAGACAATAGACAAGAACCCCTTACC	241
OY	242	tgcagctcagcagccctgtgcactctgaagacactgcgcgtctatattgt-----aatt	292
DB	242	TGCAATATCAACCGTCTGGCCGCCGAGGACACAGCCATATATCTCTGTCAAGAGACTGG	301
OY	293	tttaaggagatgcttttgactatttgggccaaggacacaggtacacgtctccctcaagt	355
DB	302	CCTGGGGAGCCCTGGTTTCTTACTTGGGGCCNAAGGGACTTGGTACTGTCTCTTCAAGCG	361
OY	353	gaagaggttcacagcgaaggtgctctgtcggtgacgtatgttttgatgaccccaaa	412
DB	352	GAGCGCGGATCCGGTGGTGGCGGATCTGAGAGGTGGCGGAAGGAGATGTCTGATGACCCAGT	421
OY	413	ctccactcactttgtcggttaccattggacaacacagccctccatctcttgaagtaagtc	472
DB	422	CTCCATTTAGTTTACCTGTCAACCCCGGAGAGCCGGCCTCCATCTTGGCAGATCTAGTC	481
OY	473	agagccctctggatagatgatatggaagaacatatgttgaattgttttcacagagccagcc	532
DB	482	AGATCATTTGTACATAGTATGGAAGAACACCTATTGATGATGATGATCTCCAGAAACAGGCC	541
OY	533	agctccaaagcgccttaactcactctgtgtctaaactgagctctggaagtcctctcagagt	592
DB	542	AGTCTCCACAGCTGCTGATCTACAAAGTTTCCAACCCGATTTTCTGGGGTCCCAACAGGT	601
OY	593	tcaactgagcagtgatcagagagacagatttcacactgaaatcaacagatggaagctgag	652
DB	602	TCAGTGGCAGTGGATCAGGAGACAGATTTCACATCAATCAAGATCAGAGAGTGGAGCTGAGG	661
OY	653	atttggaggttatattatgtcgtcggaaggttaacattctccgctcagtttggtgtcgca	712
DB	662	ACGTGGGAGTTTATTTACTGCTTTCAAGGTTTCAATGTTTCATTACGTTTGGCCAGG67TA	721
OY	713	ccaagctggaatcaaa	729
DB	722	CCAAGCTGCAATTAA	738
<p>RESULT 14</p> <p>US-08-759-804A-31</p> <p>Sequence 31, Application US/08759804A</p> <p>Patent No. 5990296</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Pastan, Ira</p> <p>APPLICANT: Willingham, Mark</p> <p>APPLICANT: Fitzgerald, David J.</p> <p>APPLICANT: Brinkmann, Ulrich</p> <p>APPLICANT: Pal, Lee</p> <p>TITLE OF INVENTION: Tumor-Specific Antibody Fragments,</p> <p>TITLE OF INVENTION: Fusion Proteins, and Uses Thereof</p> <p>NUMBER OF SEQUENCES: 68</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Townsend and Townsend and Crew LLP</p> <p>STREET: Two Embarcadero Center, Eighth Floor</p> <p>CITY: San Francisco</p> <p>STATE: California</p> <p>COUNTRY: USA</p> <p>ZIP: 94111-3834</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC Compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: Patent Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/759,804A</p> <p>FILING DATE: 03-DEC-1996</p>			

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CLASSIFICATION: 536
Prior APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
Prior APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
Prior APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..738
OTHER INFORMATION: /note="Humanized B3 single-chain Fv"
US-08-759-804A-31

Query Match: 47.9%, Score 349, DB 2, Length 738;
Best Local Similarity: 68.2%; Pred. No. 9.9e-94;
Matches 503; Conservative 0; Mismatches 225; Indels 9; Gaps 1.

OY 2 aggtcagctgtgaagcagctcgtggcgagagcctgtgagtcaggcgctcagtcagagtgct 61
DB 2 atgtgaagctgctgtgagctgtggcgagcgctgtgcagccggcgctccctgaactct 61
OY 62 cctgcagcctctgtcctcctcaacatctaaagctactatatactcagctgggtgtgacagagc 121
DB 62 cctgtgcacacccctctgattcacttcttcacagcattattactatgatttggtgtcccgagccc 121
OY 122 ctgaacagagcgctgagtgattgattgattgattgattgattgattgattgattgattgattgatt 181
DB 122 cggcgacagggcctgtgagtggtgcgcatatcattgattgattgattgattgattgattgattgatt 181
OY 182 ccccgaaagttccagggcgaagccactatgactgtcagagacacatccccaataaacgctacc 241
DB 182 cagacactgttaaaagggccgggttcacacattctcagagacatgacaaagacacacccctctacc 241
OY 242 tgcagctcagagcagctgtgacatctgagggacatcgcgtctattatgtt-----aatt 292
DB 242 tgcgaatgatacgtgtgtccgccccgagagacacacccatattatttcttgcgaagagactcg 301
OY 293 tttaacggagatcctttggaactatgtgggccaaggagacacaggttcacgcgtctcccaagt 352
DB 302 cctggcgagaccctggttgccttactgtggggcagagagacactgtgctactgtctctcagggc 361
OY 363 gaggcggttcagggcgagatgtgctctgtgcggtgtggcgagatcggatgttttgatgacccaaa 412
DB 362 gagggcgatctcggtgtgtggcgagatgtgaggtggcggaagccatgtgctgagaccact 421
OY 413 ctccacactcactgttcggtttacactatgagcaacacagccacatctctcttcaagtcaagc 472
DB 422 ctccatttgaatttactctgtcaccccgcgagagacccggcctccttcttgcacatctagtc 481
OY 473 agagcctcttgatagtgatggaagacatatltgaattgtgtgttacagagggcagggc 532
DB 482 agatcatgtgatacatgataatggaacacactattttgaaatgtaacctgcgaacacaggcc 541
OY 533 agtcccaaaaggcctaatactctcgtgtgtcctaaactggacctctgagctccctcagaagt 592
DB 541 agtcccaaaaggcctaatactctcgtgtgtcctaaactggacctctgagctccctcagaagt 592

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:22:50 ; Search time 26.51 Seconds

(without alignments)
622.401 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289

Sequence: 1 QVQLQSGAEIVRSGASVYK.....CMQGTSPDLFGAGTKLEIK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: PIR_66:**

1: p1r1:**

2: p1r2:**

3: p1r3:**

4: p1r4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912.5	70.8	249	2 S41374	single chain Fv an
2	832.5	64.6	223	2 JC5322	p53 specific singl
3	815	63.2	268	2 A56446	Ig heavy chain V r
4	560	43.4	132	2 C32513	Ig kappa chain pre
5	553	42.9	113	2 F30560	Ig kappa chain V r
6	545.5	42.3	136	2 S04576	Ig heavy chain pre
7	541	42.0	112	2 A55491	proteolytic antibo
8	539	41.8	112	2 A36259	Ig kappa chain V r
9	537	41.7	111	2 S20709	Ig kappa chain V r
10	528	41.0	116	2 S15672	Ig heavy chain V r
11	527	40.9	112	2 PLO273	Ig kappa chain V r
12	517	40.1	137	2 S52445	Ig heavy chain V r
13	511	39.6	101	2 A33730	Ig kappa chain V r
14	509.5	39.5	120	2 S03471	Ig heavy chain V-D
15	509	39.5	131	2 S31577	Ig kappa chain - m
16	505.5	39.2	118	2 S25174	Ig heavy chain V r
17	500	38.8	178	2 S29594	Ig gamma chain (NM
18	488	37.9	122	2 S06823	Ig heavy chain V r
19	487.5	37.8	117	2 S1786	Ig heavy chain V r
20	485.5	37.7	120	2 S03484	Ig heavy chain V-D
21	479.5	37.2	221	2 S49220	Ig gamma-1 chain -
22	476	36.9	133	2 S2330	Ig kappa chain pre
23	476	36.9	142	2 S22902	Ig gamma chain V r
24	475.5	36.9	116	2 S24289	Ig heavy chain V r
25	474.5	36.8	115	2 S03482	Ig heavy chain V-D
26	474	36.8	103	2 PH1055	Ig light chain V r
27	473	36.7	133	2 S42611	HUNTK protein prec
28	472	36.6	133	2 S40324	Ig kappa chain V r
29	471	36.5	108	2 PH1012	Ig heavy chain V r

30	469	36.4	91	2 S42186	Ig kappa chain V r
31	469	36.4	133	1 K2HUP	Ig kappa chain pre
32	468.5	36.3	140	2 S22658	Ig kappa chain pre
33	465	36.1	103	2 PH1056	Ig light chain V r
34	464.5	36.0	144	2 B30502	Ig heavy chain V r
35	463	35.9	118	2 S40374	Ig heavy chain - h
36	462	35.8	114	4 A47271	nitrophenyl phosph
37	461	35.8	133	1 A24452	Ig kappa chain pre
38	460.5	35.7	114	2 B49002	Ig kappa chain V r
39	460	35.7	112	2 A31807	Ig kappa chain V r
40	458.5	35.6	114	2 S43572	Ig kappa chain pre
41	453	35.1	122	2 S40338	Ig kappa chain - h
42	451	35.0	131	2 B39276	Ig light chain pre
43	450	34.9	115	2 S38715	Ig kappa chain V r
44	449	34.8	132	2 S40322	Ig kappa chain - h
45	447	34.7	112	2 S38719	Ig light chain V r

ALIGNMENTS

```
RESULT 1
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C/Accession: S41374
R:Artsekeno, O.; Weller, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti
A:Reference number: S41374
A:Accession: S41374
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:229480

Query Match          70.8%; Score 912.5; DB 2; Length 249;
Best Local Similarity 72.5%; Pred. No. 3.3e-58;
Matches 179; Conservative 25; Mismatches 38; Indels 5; Gaps 2;

QY 1 QVQLQSGAEIVRSGASVYKLSCTASGFNIRKDYMHMKRPEQGLEWIGIDPENGDTGY 60
   |||||
DB 1 QVQLQSGAEIVRSGASVYKLSCTASGFNIRKDYMHMKRPEQGLEWIGIDPENGDTGY 60
   |||||

QY 61 APRFQKATMTADTSSNTAVYQLSLASEDTAVYCC---NFYGDALDWGGCTTYVSS 116
   |||||
DB 61 APRFQKATMTADTSSNTAVYQLSLASEDTAVYCC---NFYGDALDWGGCTTYVSS 116
   |||||

QY 117 GGGSGGGSGGGSGGGSDYLMQGTPLTISVTIGOPASISCKSSOSLSDSDGKTYLNLQRP 176
   |||||
DB 120 RGGSGGGSGGGSGGGSDYLMQGTPLTISVTIGOPASISCKSSOSLSDSDGKTYLNLQRP 176
   |||||

QY 177 GOSPKRLIYVSKLSDGVPDRFGSGSGDTFTLKIRNVEAEDGVYVCMQGTSPDLFGA 236
   |||||
DB 180 GOSPKRLIYVSKLSDGVPDRFGSGSGDTFTLKIRNVEAEDGVYVCMQGTSPDLFGA 236
   |||||

QY 237 GTKLEIK 243
   |||||
DB 240 GTKLEIK 246
   |||||

RESULT 2
JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C>Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C/Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MID:97168950
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A:Accession: J05322
 A:Molecule type: mRNA
 A:Residues: 1-233 <TAN>
 A:Experimental source: hybridoma cell
 C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 64.6%; Score 832.5; DB 2; Length 233;
 Best Local Similarity 68.9%; Pred. No. 1.5e-52;
 Matches 164; Conservative 25; Mismatches 44; Indels 5; Gaps 3;

QY 5 QQSAAELVRSASVKSCTASGFNINQDYMHVWKPQEGLEWIGMDPENGDTEYAPKF 64
 DB 1 QESAAELVRSASVKSCTASGFNINQDYMHVWKPQEGLEWIGMDPENGDTEYAPKF 60
 QY 65 QGKATMTADTSSNTAYTOLSLASEDTAVYYCNFYGDALDWMGGGTYYTVSSGGSGGG 124
 DB 61 GVRATMTADTSSNTAYTOLSLASEDTAVYYCNFYGDALDWMGGGTYYTVSSGGSGGG 117
 QY 125 GSGGGSDVLTOTPLTSLVTIGOPASISCKSSQSLSDSGKTYLNLORPQSPKRLI 184
 DB 118 ASGGGGSDIELTQSPALVSLGORATISCRASKS-VTSGSYMHNMNQKPGQPPRLI 176
 QY 185 YLVSKLSDGVPRDTGSGSDFTLTKINRYEADLVGYVCMOGTHSPLEAGTKLEI 242
 DB 177 YLVNLSGVPARFSGSGSDFTLTKINRYEADLVGYVCMOGTHSPLEAGTKLEI 233

RESULT 3

A56446
 Ig heavy chain V region (3H-3H scfv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)
 C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
 C:Accession: A56446
 R:Lang: P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.
 J. Biol. Chem. 270, 7829-7835, 1995
 A:Title: A high affinity diognin-binding protein displayed on M13 is functionally identical
 A:Reference number: A56446; M0ID:95229583
 A:Accession: A56446
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-268 <TAN>
 A:Cross-references: GB:020617
 C:Keywords: heterotetramer; Immunoglobulin

Query Match 63.2%; Score 815; DB 2; Length 268;
 Best Local Similarity 64.5%; Pred. No. 3.2e-51;
 Matches 138; Conservative 30; Mismatches 49; Indels 8; Gaps 3;

QY 1 QVQLQSGAEIVRSASVKSCTASGFNINQDYMHVWKPQEGLEWIGMDPENGDTEY 60
 DB 3 QVQLQSGAEIVRSASVKSCTASGFNINQDYMHVWKPQEGLEWIGRIAPANGTKY 62
 QY 61 APRFQGAATMTADTSSNTAYTOLSLASEDTAVYYC-NFYGDALD-YWGGTYYTVSSGG 118
 DB 63 DPFQGAATMTADTSSNTAYTOLSLASEDTAVYYCASYLTREYTWGGTYYTVSSGG 122
 QY 119 GSGGGSDVLTOTPLTSLVTIGOPASISCKSSQSLSDSGKTYLNLORPQSPKRLI 178
 DB 123 GSGGGSDVLTOTPLTSLVTIGOPASISCKSSQSLSDSGKTYLNLORPQSPKRLI 176
 QY 179 SPRLIYVSKLSDGVPRDTGSGSDFTLTKINRYEADLVGYVCMOGTHSPLEAGTK 238
 DB 177 SPRLIYVSKLSDGVPRDTGSGSDFTLTKINRYEADLVGYVCMOGTHSPLEAGTK 236
 QY 239 KLEIK 243
 DB 237 KLEIK 241

RESULT 4

Ig kappa chain precursor V region (BXMI4) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
 C:Accession: C32513
 R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.
 J. Clin. Invest. 82, 852-860, 1988
 A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
 A:Reference number: N94689; M0ID:88311394
 A:Accession: C32513
 A:Molecule type: DNA
 A:Residues: 1-113 <KOF>
 A:Cross-references: GB:M20830; NID:q196939; PIDN:AAA8844.1; PID:q196940
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:36-115/Domain: Immunoglobulin homology <IMM>

Query Match 43.4%; Score 560; DB 2; Length 132;
 Best Local Similarity 95.5%; Pred. No. 2.1e-33;
 Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 132 DVLTOTPLTSLVTIGOPASISCKSSQSLSDSGKTYLNLORPQSPKRLIYVSKLD 191
 DB 21 DVLTOTPLTSLVTIGOPASISCKSSQSLSDSGKTYLNLORPQSPKRLIYVSKLD 80
 QY 192 SGVPDRFTGSGSDFTLTKINRYEADLVGYVCMOGTHSPLEAGTKLEI 243
 DB 81 SGVPDRFTGSGSDFTLTKINRYEADLVGYVCMOGTHSPLEAGTKLEI 132

RESULT 5
 F30560
 Ig kappa chain V region (28.4.10A) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
 C:Accession: F30560
 R:Matsuda, T.; Kabat, E.A.
 J. Immunol. 142, 865-870, 1989
 A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono

A:Reference number: A30560; M0ID:89110062
 A:Accession: F30560
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <MAT>
 A:Cross-references: NID:M24273; NID:q197081; PIDN:AAA63370.1; PID:q197082
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:16-95/Domain: Immunoglobulin homology <IMM>

Query Match 42.9%; Score 553; DB 2; Length 113;
 Best Local Similarity 94.6%; Pred. No. 5.5e-33;
 Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 132 DVLTOTPLTSLVTIGOPASISCKSSQSLSDSGKTYLNLORPQSPKRLIYVSKLD 191
 DB 1 DVLTOTPLTSLVTIGOPASISCKSSQSLSDSGKTYLNLORPQSPKRLIYVSKLD 60
 QY 192 SGVPDRFTGSGSDFTLTKINRYEADLVGYVCMOGTHSPLEAGTKLEI 243
 DB 61 SGVPDRFTGSGSDFTLTKINRYEADLVGYVCMOGTHSPLEAGTKLEI 112

RESULT 6
 S04576
 Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
 C:Accession: S04576
 R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;
 Eur. J. Immunol. 17, 91-95, 1987
 A:Title: Molecular analysis of the murine lupus-associated anti-self response: involv

A:Reference number: S04573; MUID:87133856
 A:Accession: S04576
 A:Molecule type: mRNA
 A:Residues: 1-136 <KOP>
 A:Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA3277.1; PID:g52030
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 545.5; DB 2; Length 136;
 Best Local Similarity 88.9%; Pred. No. 2,3e-32;
 Matches 104; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVLOQSGAEIVRSGAVKSLCTAGSFNIKDYMMWVKORPEOGLEWICWIDPENGDTLY 60
 :|||||
 Db 20 EVLOQSGAEIVRSGAVKSLCTAGSFNIKDYMMWVKORPEOGLEWICWIDPENGDTLY 79

QY 61 ARFQKATMTADTSNTAYLQISLASDPAVYCNFYGD-ALDWGSGTWTYSS 116
 :|||||
 Db 80 ASKFGKATMTADTSNTAYLQISLASDPAVYCYTTGAYAMDYWGSGTWTYSS 136

RESULT 7
 A55491
 proteolytic antibody light chain - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 21-Jan-2000
 C:Accession: A55491

R:Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.
 J. Biol. Chem. 269, 33389-33393, 1994

A:Title: Molecular cloning of a proteolytic antibody light chain.

A:Reference number: A55491; MUID:95096089

A:Accession: A55491

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <GAO>

A:Cross-references: GB:L34775

A:Note: authors translated the codon TAT for residue 37 as Thr

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 42.0%; Score 541; DB 2; Length 112;
 Best Local Similarity 92.9%; Pred. No. 3,9e-32;
 Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 132 DVLMQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 191
 :|||||
 Db 1 DVVMQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 60

QY 192 SGVDPRTGSGSGTDFTLKINRVEAEDLGYYVCMQGTSPLEFGAGTKLEIK 243
 :|||||
 Db 61 SGVDPRTGSGSGTDFTLKINRVEAEDLGYYVCMQGTSPLEFGAGTKLEIK 112

RESULT 8

A36259

Ig kappa chain V region (TE34) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000

C:Accession: A36259

R:Zilber, B.; Scherf, T.; Levitt, M.; Anglistter, J.

Biochemistry 29, 10032-10041, 1990

A:Title: NMR-derived model for a peptide-antibody complex.

A:Reference number: A36259; MUID:91104915

A:Accession: A36259

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-112 <ZIL>

A:Cross-references: GB:M30458; GB:M30459; GB:M30480; GB:M30481; GB:M30482; GB:M30483

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 41.8%; Score 539; DB 2; Length 112;
 Best Local Similarity 92.9%; Pred. No. 5,4e-32;
 Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 132 DVLMQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 191
 :|||||
 Db 1 DVVMQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 60

QY 192 SGVDPRTGSGSGTDFTLKINRVEAEDLGYYVCMQGTSPLEFGAGTKLEIK 243
 :|||||
 Db 61 SGVDPRTGSGSGTDFTLKINRVEAEDLGYYVCMQGTSPLEFGAGTKLEIK 112

RESULT 9
 S20709

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C:Accession: S20709

R:Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.;

submitted to the EMBL Data Library, April 1992

A:Description: Binding specificity and variable region sequences of two monoclonal an

A:Reference number: S20706

A:Accession: S20709

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-111 <BRE>

A:Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA77975.1; PID:g52656

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; Immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 537; DB 2; Length 111;
 Best Local Similarity 91.9%; Pred. No. 7,5e-32;
 Matches 102; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 132 DVLMQTPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 191
 :|||||
 Db 1 DIQLTQSPPLTISVTIGOPASISCKSSQSLSDSGKTYLNMWLQRPQSPKRLIYVSKLD 60

QY 192 SGVDPRTGSGSGTDFTLKINRVEAEDLGYYVCMQGTSPLEFGAGTKLEIK 242
 :|||||
 Db 61 SGVDPRTGSGSGTDFTLKINRVEAEDLGYYVCMQGTSPLEFGAGTKLEIK 111

RESULT 10
 S15672

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S15672

R:Tempest, P.R.; Brenner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harri

Bio/Technology 9, 265-271, 1991

A:Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial

A:Reference number: S15672; MUID:91337412

A:Accession: S15672

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-116 <TEM>

A:Cross-references: EMBL:X58835; NID:g51978; PIDN:CAA41644.1; PID:g51979

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.0%; Score 528; DB 2; Length 116;
 Best Local Similarity 84.3%; Pred. No. 3,4e-31;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:23:24 ; Search time 16.14 Seconds

(without alignments)
486.212 Million cell updates/sec

Title: US-09-297-181-2

Sequence: 1 QVQLQSGAEIVRSQASVYKL.....CMQGTSPLETFGAGTKLEIK 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt-39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469	36.4	133	1	KV2F_HUMAN
2	428	33.2	113	1	KV2B_HUMAN
3	428	33.2	113	1	KV2D_HUMAN
4	428	33.2	113	1	KV2G_MOUSE
5	423	32.8	117	1	KV2E_HUMAN
6	423	32.8	117	1	HV07_MOUSE
7	418.5	32.5	115	1	KV2A_HUMAN
8	405.5	31.5	120	1	HV03_MOUSE
9	399	31.0	137	1	HV01_MOUSE
10	397.5	30.8	140	1	HV02_MOUSE
11	396.5	30.8	112	1	KV2C_HUMAN
12	384.5	29.8	117	1	HV12_MOUSE
13	384	29.8	113	1	HV1C_HUMAN
14	382	29.6	113	1	KV2C_MOUSE
15	382	29.6	113	1	KV2F_MOUSE
16	380.5	29.5	117	1	HV13_MOUSE
17	380	29.5	118	1	HV51_MOUSE
18	378	29.3	112	1	KV2A_MOUSE
19	377	29.2	113	1	KV3E_MOUSE
20	377	29.2	120	1	HV50_MOUSE
21	375.5	29.1	138	1	HV48_MOUSE
22	372.5	28.9	111	1	KV3N_MOUSE
23	372.5	28.9	116	1	HV15_MOUSE
24	371	28.8	112	1	KV2D_MOUSE
25	367.5	28.5	111	1	KV3M_MOUSE
26	367.5	28.5	111	1	HV3I_MOUSE
27	365.5	28.4	108	1	KV1_CANFA
28	365.5	28.4	111	1	KV3O_MOUSE
29	364	28.2	117	1	HV09_MOUSE
30	363.5	28.0	111	1	KV3J_MOUSE
31	360.5	28.0	111	1	KV3Q_MOUSE
32	359	27.9	110	1	KV3P_MOUSE
33	358.5	27.8	134	1	KV4C_HUMAN

34	358	27.8	117	1	HV06_MOUSE
35	352	27.3	117	1	HV04_MOUSE
36	352	27.3	117	1	HV49_MOUSE
37	351	27.2	117	1	HV1A_HUMAN
38	350.5	27.2	111	1	KV3U_MOUSE
39	350.5	27.2	114	1	KV4A_HUMAN
40	349.5	27.1	111	1	KV3K_MOUSE
41	348.5	27.0	111	1	KV3S_MOUSE
42	348	27.0	117	1	HV10_MOUSE
43	348	27.0	117	1	HV52_MOUSE
44	347.5	27.0	111	1	KV3H_MOUSE
45	345.5	26.8	131	1	KV3I_MOUSE

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	Length
1	KV2F_HUMAN	QVQLQSGAEIVRSQASVYKL.....CMQGTSPLETFGAGTKLEIK 243			133 AA
AC	P06310:				
DT	01-JAN-1988	(Rel. 06, last sequence update)			
DT	01-JAN-1988	(Rel. 06, last sequence update)			
DT	15-JUL-1999	(Rel. 38, last annotation update)			
DE	IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=86041852; PubMed=2997711;				
RX	Klobeck H.G., Meisel A., Combratio G., Solomon A., Zachau H.G.;				
RT	"Human immunoglobulin kappa light chain genes of subgroups II and III."				
RL	Nucleic Acids Res. 13:6499-6513(1985).				
CC	-----				
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CC	or send an email to license@sib-sib.ch).				
DR	EMBL: 2000020; CAAT7315.1; -				
DR	PIR: A01890; K2HUP.				
DR	INTERPRO: IPR003006; -				
DR	PFAM: PF00047; 19; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL	1	20		
FT	CHAIN	21	133		
FT	DOMAIN	21	43		
FT	DOMAIN	44	59		
FT	DOMAIN	60	74		
FT	DOMAIN	75	81		
FT	DOMAIN	82	113		
FT	DOMAIN	114	132		
FT	DOMAIN	123	132		
FT	DISULFID	43	113		
FT	NON_TER	133	133		
SQ	SEQUENCE	133 AA; 14707 MW; 5130CAR3673009EE CRC64;			

Query Match 36.4%; Score 469; DB 1; Length 133;

Best Local Similarity 76.7%; Pred. No. 2.5e-29;

Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

128 GGSVDVLMQPTPLTSLVITIGOPASISCKSSQSLDSDKTYLWLLRGOSPKRLITLV 187

17 GSSGDVLMQPTPLTSLVITIGOPASISCKSSQSLDSDKTYLWLLRGOSPKRLITLV 76

188 SKLSDGVPRFTGSGSGTDFTLKINRVEADLGVYCMQGTSPLETFGAGTKLEIK 243

Db 77 SNRSGVPDRFSGSGSDFTLTKISRYEADGVYICMGTHMSWTFGGTKVEIK 132

RESULT 2

KV2B_HUMAN STANDARD; PRT; 113 AA.

AC P01615;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION FR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE=76253627; PubMed=821524;

RA Riessen W.F., Jaton J.C.;

RT "Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";

RL Biochemistry 15:3829-3833(1976).

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.

CC PIR; A01886; K2H0R.

DR INTERPRO; IPR003006; -.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 40 54 FRAMEWORK 2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 62 93 FRAMEWORK 3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 103 112 FRAMEWORK 4.

FT DISULFID 23 93 BY SIMILARITY.

FT NON_TER 113 113

SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 33.2%; Score 428; DB 1; Length 113;

Best Local Similarity 71.4%; Pred. No. 2.7e-26;

Matches 80; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 132 DVMTQPTPLTSLVIGQPASISCKSSQSLSDSGKTYLMLLQRPQSPKRLIYLVSRLD 191

Db 1 DVMTQSPFLPTLGPASISCKSSQSLVYRBGTYLBMWLYLQKPGSPFLIYALSNRA 60

QY 192 SGVPDRFSGSGSDFTLTKINRYEADGVYICMGTHMSWTFGGTKVEIK 243

Db 61 SGVPDRFSGSGSDFTLTKIRVQAEADVGYICMGATZSPYTFGGTKLZIK 112

RESULT 3

KV2D_HUMAN STANDARD; PRT; 113 AA.

ID KV2D_HUMAN

AC P01617;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION TEW.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RN [1]

RP SEQUENCE (BENCE-JONES PROTEIN TEW).

RX MEDLINE=7418480; PubMed=4596148;

RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;

RT "Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloidosis.";

RL Biochemistry 12:3763-3780(1973).

RN [2]

RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).

RX MEDLINE=7316638; PubMed=4700495;

RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,

RA Glenner G.G.;

RT "Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";

RL J. Clin. Invest. 52:1276-1281(1973).

CC -I- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.

CC -I- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.

CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

CC PIR; A01886; K2H0T.

DR INTERPRO; IPR003006; -.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region; Bence-Jones protein; Amyloid.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 40 54 FRAMEWORK 2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 62 93 FRAMEWORK 3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 103 112 FRAMEWORK 4.

FT DISULFID 23 93 BY SIMILARITY.

FT NON_TER 113 113

SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 33.2%; Score 428; DB 1; Length 113;

Best Local Similarity 71.4%; Pred. No. 2.7e-26;

Matches 80; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 132 DVMTQPTPLTSLVIGQPASISCKSSQSLSDSGKTYLMLLQRPQSPKRLIYLVSRLD 191

Db 1 DVMTQSPFLPTLGPASISCKSSQSLSDSGKTYLMLLQRPQSPKRLIYLVSRLD 60

QY 192 SGVPDRFSGSGSDFTLTKINRYEADGVYICMGTHMSWTFGGTKVEIK 243

Db 61 SGVPDRFSGSGSDFTLTKISRYEADGVYICMGALQAPITFGGTRLEIK 112

RESULT 4

KV2G_MOUSE STANDARD; PRT; 113 AA.

ID KV2G_MOUSE

AC P01631;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION 26-10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE.

RX STRAIN-A/J;

RX MEDLINE=83178921; PubMed=6404298;

RA Novotny J., Margolies M.N.;

RT "Amino acid sequence of the light chain variable region from a mouse anti-dioxin hybridoma antibody.";

RL Biochemistry 22:1153-1158(1983).

CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ICG2A HYBRIDOMA PROTEIN THAT BINDS DIOXIN.

CC PIR; A01914; KVM26.

DR INTERPRO; IPR003006; -.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.

FT DOMAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 40 54 FRAMEWORK 2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 62 93 FRAMEWORK 3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 103 112 FRAMEWORK 4.

FT DISULFID 23 93 BY SIMILARITY.

FT .NON_TER 113 113
SQ SEQUENCE 113 AA: 12273 MW: F9F39CE949A84C2A CRC64:

Query Match
Best Local Similarity 74.1%; Pred. No. 2.7e-26;
Matches 83; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 132 DYLMOTPTLTSTVIGOPASISCKSSQSLDSDGKTYLNMLOPQSGPKRLIYVSKLD 191
DB 1 DVMYOTPTSLVSTLSDQASISCKSSQSLVHSGNTYLMWYLOKAGQSKLLIYKVSNEF 60
OY 192 SCVPPRFSGSGGTDFTLKINRYEADLVGYTCWQTHSPFTGACTKLEIK 243
DB 61 SCVPPRFSGSGGTDFTLKINRYEADLVGYTCWQTHSPFTGACTKLEIK 112

RESULT 5
KV2E_HUMAN STANDARD: PRT; 117 AA.
AC P06309:
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION GM607 PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-84191506; PubMed-6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity"; 309:73-76(1984).

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CC EMBL: 200009; NOT_ANNOTATED_CDS.
DR PIR: A01889; K2HUGM.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK 1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 58 FRAMEWORK 2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 66 97 FRAMEWORK 3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 107 116 FRAMEWORK 4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA: 12664 MW: 92C57DC719E558B1 CRC64:

Query Match
Best Local Similarity 32.8%; Score 423; DB 1; Length 117;
Matches 81; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

OY 128 GGSQDVLMTGPTLTSTVIGOPASISCKSSQSLDSDGKTYLNMLOPQSGPKRLIYV 187
DB 1 GGSQDVLMTGPTLTSTVIGOPASISCKSSQSLDSDGKTYLNMLOPQSGPKRLIYV 60
OY 188 SKLDGVPDRFTGSGSGTDFTLKINRYEADLVGYTCWQTHSPFTGACTKLEIK 243

DB 61 SNRAGVDPDRFSGSGGTDFTLKINRYEADLVGYTCWQTHSPFTGACTKLEIK 116

RESULT 6
HV07_MOUSE STANDARD: PRT; 139 AA.
AC P01751; P01752; -
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C57BL/6;
RA MEDLINE-81234548; PubMed-6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).

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CC or send an email to license@sib-sib.ch).

CC EMBL: J00529; AAA8170.1; -
DR PIR: A02034; MHM818.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1
FT SIGNAL 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139
SQ SEQUENCE 139 AA: 15419 MW: 1B57DD4FD0C9F465 CRC64:

Query Match
Best Local Similarity 32.8%; Score 423; DB 1; Length 139;
Matches 81; Conservative 15; Mismatches 20; Indels 4; Gaps 2;

OY 1 OVOLOOAGAEIVRSGASYKLSCTAGSFNIKIDYMHVQRQPGLEWIGWIDPENGDEY 60
DB 20 OVOLOOAGAEIVRSGASYKLSCTAGSFNIKIDYMHVQRQPGLEWIGWIDPENGDEY 79
OY 61 APKFGKATMTADISSNATYLOLSSLASADPAVYIC---NFTGDA-LDYWGQGITVYSS 116
DB 80 NKFPSKATLTLYDKPSSATYMOSSLTSEDSAVYVCARYDYGSSYPYWGQGITLVSS 139

RESULT 7
KV2A_HUMAN STANDARD: PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)

[illegible]

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RA DREYER W.J., GHAY W.R., HOOD L.E.:
RT "The genetic, molecular, and cellular basis of antibody formation:
RL some facts and a unifying hypothesis."
CC Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01887; K2HML.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 1.
FW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 53 FRAMEWORK 2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 61 FRAMEWORK 3.
FT DOMAIN 6 92 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 7 93 FRAMEWORK 4.
FT DISULFID 102 111 BY SIMILARITY.
FT NON_TER 23 92
FT SEQUENCE 112 112
SO QUERY MATCH 30.8%; SCORE 396.5; DB 1; LENGTH 112;
BEST LOCAL SIMILARITY 63.4%; PRED. NO. 6.6e-24;
MATCHES 71; CONSERVATIVE 25; MISMATCHES 15; INDELS 1; GAPS 1
QY 132 DVLMTQPTLTSVTIGIGPASICSKSSQSLDSDGKTYLNLMLLPQSPKRLIYVSKLD 191
DB 1 DIVLQSPSLPLVTGEPASISCRSSQNLNLZBSGB-YLDWVLYZKPKSPZSLZLIYGSNNA 59
QY 192 SCVDPRTFGSGSGDTFTLKINRVEADLCYVCCWQGTSHLPFGAGTKLEIK 243
DB 60 SCVPRFSGS3SGTBTFTLKISRVAZABGVVYCCMALQPLTFGGGTNVEIK 111
RESULT 12
HV12_MOUSE ;
HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1G HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC [1]
RP SEQUENCE.
RX MEDLINE=83075347; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RL heavy chain constant region domains."
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC PIR: A02039; M4M54E.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 1.
FW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
FT SEQUENCE 117 117
SO QUERY MATCH 29.8%; SCORE 384.5; DB 1; LENGTH 117;
BEST LOCAL SIMILARITY 65.0%; PRED. NO. 5.6e-23;
MATCHES 76; CONSERVATIVE 12; MISMATCHES 28; INDELS 1; GAPS 1
QY 1 OV0LQSGAEIVRSAGSVKSLCTASGFINIKDYMHMVYKORPEQGLGEMIGWIDPENGDTLEY 60

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Db      1 EVOLQOQSGPFLVPGASVKKMSCKASGYTFDYMKWVKQSHGKSLIEWIGINPNNGCTSY 60
        61 APPFGKATMTADTSSNTATVLOLSSLASSEPTAYVC-NFGDMLDYGGGTTTVSS 116
        61 NQFKGKATLTVDKSSSTAYMQLNLSIEDSAVYCAKRDYMTFVWGAGTTTVSS 117

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RESULT 13
HYLC_HUMAN STANDARD; PRT; 143 AA.

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AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 HEAVY CHAIN V-I REGION ND PRECURSOR (FRAGMENTS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 16-142.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
DR PIR; A02026; EIHUND.
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT FT NON_CONS 4 5
FT SGNL 1 15
FT CHAIN 16 143 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 16 16 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 37 111
FT CONFLICT 17 17 T -> V (IN REF. 2).
FT CONFLICT 49 50 IH -> HI (IN REF. 2).
FT CONFLICT 63 64 VG -> GV (IN REF. 2).
FT CONFLICT 121 121 MISSING (IN REF. 2).
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16051 MW; DE80DD280D002027E CRC64;

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Query Match      29.8%; Score 384; DB 1; Length 143;
Best Local Similarity 56.2%; Pred. No. 7.7e-23;
Matches 72; Conservative 18; Mismatches 26; Indels 12; Gaps 2;

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QY 1 QVQLQSGALVPSGASVKLSCTASGFNIRKYYMWVKORPEQGLEWIGMIDENGPTEY 60
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 16 QVQLQSGALVPSGASVKLSCTASGFNIRKYYMWVKORPEQGLEWIGMIDENGPTEY 75
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 APPFGKATMTADTSSNTATVLOLSSLASSEPTAYVC-----NF-YGDAIDYWGQ 108
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 76 APPFGKATMTADTSSNTATVLOLSSLASSEPTAYVC-----NF-YGDAIDYWGQ 135
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 109 GTTVTVSS 116
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 136 GTTVTVSS 143

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RESULT 14
KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 KAPPA CHAIN V-II REGION MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphoricholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORICHOCHOLINE.
DR PIR; A01910; KVM51.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region.
FT FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 FRAMEWORK 2.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

```

```

Query Match      29.6%; Score 382; DB 1; Length 113;
Best Local Similarity 67.0%; Pred. No. 8.4e-23;
Matches 75; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

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QY 132 DVLTQTPPLTISTIQPASICSSQSLSDSGKTYLNLQRPQSPKRLTYLSKLD 191
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DIYTDLSKPTSGESVISICRSSLKLYKDKTYLWFLDGPQSPPLTYLWSTRA 60
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 SGVSDPFTSGSGTDFTLKINRVEADLGYVCCGTHSTPLFPGAGTKLEIK 243
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 SGVSDPFTSGSGTDFTLKINRVEADLGYVCCGTHSTPLFPGAGTKLEIK 112
    I : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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RESULT 15
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 15 KAPPA CHAIN V-II REGION 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoozobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.

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FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 29.68; Score 382; DB 1; Length 113;
Best Local Similarity 67.0%; Pred. No. 8.4e-23;
Matches 75; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

OY 132 DVLMTOTPLFLSYTIGOPASISCKSSQSLDSOGKTYLNLORPGOSPRLIYLVSKLD 191
DB 1 DIVMTQTAPSAALVTPGESVSISCRSSKSLHNSGNTLYLNFLORPQCCPOLLIYRMSNLA 60
OY 192 SGVPDRFTSGSGSGTDFTLKINRYEAEDLGYYCWOGTSPITFGAGTKLEIK 243
DB 61 SGVPDRFTSGSGSGTAFPLRISRYEAEDVGYYCWOGTREPYTFGGTKLEIK 112

Search completed: February 12, 2001, 15:26:39
Job time: 195 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2001, 15:22:50 ; Search time 42.85 Seconds
(without alignments)
664,680 Million cell updates/sec

Title: US-09-297-181-2
Perfect score: 1289
Sequence: 1 QVQLQSGAEIVRSAGASYKL.....CMQGTSPILFPGAGTKLEIK 243

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP.TREMBL_15:*
2: SP.Archea:*
3: SP.Bacteria:*
4: SP.fungi:*
5: SP.human:*
6: SP_invertebrate:*
7: SP.mhcn:*
8: SP.Organelle:*
9: SP.phage:*
10: SP.plant:*
11: SP.Rodent:*
12: SP.virus:*
13: SP.vertibrate:*
14: SP.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696.5	54.0	298	11 Q9YF0	Q9YF0 mus musculi
2	447.5	34.7	114	09UL80	Q9UL80 homo sapien
3	443.5	34.4	109	11 Q9UL85	Q9UL85 mus musculi
4	428	33.2	118	11 Q9ULC4	Q9ULC4 mus musculi
5	401.5	31.1	117	11 Q9QX9	Q9QX9 mus musculi
6	396.5	30.8	117	11 Q9QXFO	Q9QXFO mus musculi
7	393.5	30.5	125	4 Q9UL95	Q9UL95 homo sapien
8	393	30.5	104	11 Q9UL82	Q9UL82 mus musculi
9	390	30.3	124	4 Q9UL92	Q9UL92 homo sapien
10	385.5	29.9	119	4 Q9UL94	Q9UL94 homo sapien
11	384	29.8	114	11 Q9UL81	Q9UL81 mus musculi
12	381	29.6	109	11 Q9UL75	Q9UL75 mus musculi
13	372	28.9	110	11 Q9UL77	Q9UL77 mus musculi
14	367.5	28.5	150	4 Q9Y298	Q9Y298 homo sapien
15	354.5	27.5	117	11 Q9ULC6	Q9ULC6 mus musculi
16	352	25.8	110	11 Q9UL83	Q9UL83 mus musculi
17	330.5	25.6	157	4 Q9S978	Q9S978 homo sapien
18	326	25.3	109	4 Q9UL78	Q9UL78 homo sapien
19	320	24.8	116	4 Q9UL89	Q9UL89 homo sapien

20	317.5	24.6	113	4 Q9UL90	Q9UL90 homo sapien
21	311	24.1	107	4 Q9UL81	Q9UL81 homo sapien
22	310.5	24.1	121	4 Q9UL71	Q9UL71 homo sapien
23	309.5	24.0	108	4 Q9UL77	Q9UL77 homo sapien
24	309.5	24.0	116	4 Q9UL93	Q9UL93 homo sapien
25	305.5	23.7	108	4 Q9UL70	Q9UL70 homo sapien
26	305.5	23.7	114	11 Q9UL85	Q9UL85 mus musculi
27	302.5	23.5	131	4 Q9UL88	Q9UL88 homo sapien
28	301	23.4	147	4 Q9Y509	Q9Y509 homo sapien
29	298	23.1	109	4 Q9UL86	Q9UL86 homo sapien
30	297	23.0	118	4 Q9UL72	Q9UL72 homo sapien
31	296.5	22.8	108	4 Q9UL79	Q9UL79 homo sapien
32	294	22.8	118	4 Q9UL91	Q9UL91 homo sapien
33	293	22.7	122	4 Q9UL84	Q9UL84 homo sapien
34	292	22.7	106	5 Q9UL10	Q9UL10 schistosoma
35	291	22.6	124	6 Q9UL06	Q9UL06 cryctolaus
36	289.5	22.5	102	11 Q9UL79	Q9UL79 mus musculi
37	289.5	22.5	103	11 Q9UL80	Q9UL80 mus musculi
38	289.5	22.5	108	4 Q9UL83	Q9UL83 homo sapien
39	289	22.4	124	6 Q9UL04	Q9UL04 cryctolaus
40	288	22.3	150	4 Q9S973	Q9S973 homo sapien
41	286.5	22.2	119	4 Q9UL73	Q9UL73 homo sapien
42	285	22.1	109	4 Q9UL85	Q9UL85 homo sapien
43	282.5	21.9	99	11 Q9UL74	Q9UL74 mus musculi
44	274	21.3	437	11 Q9UL14	Q9UL14 mus musculi
45	268.5	20.8	104	4 Q9UL87	Q9UL87 homo sapien

ALIGNMENTS

RESULT 1
ID Q9YF0 PRELIMINARY: PRT; 298 AA.
AC Q9YF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CN 8 SCFV.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; ISSUE-SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RT Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phase display subtraction
RT method *;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB036341; BAA86633.1; -;
DR HSSP: P01607; IREL.
DR INTERPRO: IPR003006; -;
DR PFM: PFM0047; Iq; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 54.0%; Score 696.5; DB 11; Length 298;
Best Local Similarity 53.3%; Pred. No. 2.9e-54;
Matches 131; Conservative 43; Mismatches 63; Indels 9; Gaps 3;

QY 1 QVQLQSGAEIVRSAGASYKLCTAGSFNKKDYMMHYKRPDQGLWIMQIPENDITF 60
DB 40 QVQLQSGGGGVKPGGSLTSCAASGSDPSRYWMSVWRAKPGGLGELWIMPDSTINY 99
QY 61 APTFOCKATMTADTSNTAYVLQSLASIEDTAVVYC---NFGDALDYMGCGTTVTVSSG 117

QY	Db	100	TPSLDKRFLISDNKNTLTYLQSKVRSBEDTALYICARASVYGHSA-XMGQGTFTVTSVG	158
QY	118	GGGSGGGGGGGGGG	SVLMTQTPLTLSVTITGQRPASISCKSSQSLDSBDGTYTLNWLQRP	177
Db	159	GGGSGGGGGGGGGG	SDIELTQSPASLSASVGEVTVITCRASGNI-----HNYLAWYQOKOG	213
QY	178	QSPKRLIVSKLSDGVPDRFTFGSSGTFETLKINRVEAEDLGYYVCWOGTHSPPLTFGAG	237	
Db	214	KSPQLLYVNAKTLAAGVPSRFSGSGSGGTGYSLKINSIQEDPDGSIYCCQHFMTPTTFGGG	273	
QY	238	TKLEIK	243	
Db	274	TKLEIK	279	
RESULT	2			
Q9UL80	PRELIMINARY:	PRT:	114 AA.	
AC	Q9UL80:			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clín. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL: AF035034; AAD56270.1; -			
DR	INTERPRO: IPR003006; -			
FT	PEAM; PF00047; 19; 1.			
FT	NON_TER	1		
FT	NON_TER	114		
SO	SEQUENCE	114 AA; 12775 MW; 070E31E210DICB01 CRC64;		
Query Match	34.7%;	Score 447.5;	DB 4;	Length 114;
Best Local Similarity	77.0%;	Pred. No. 1.2e-32;		
Matches	87;	Conservative 11;	Mismatches 14;	Indels 1;
QY	132	DVLMTQTPLTLSVTITGQRPASISCKSSQSLDSBDGTYTLNWLQRPQSPKRLIVLSKLD	191	
Db	1	DVMTQSPSLSPYTLRQPASISCKSSQSPVYSDGTYTLNWLQFPQRPQSPKRLIVLSNRD	60	
QY	192	SGVDRFTFGSSGSDFTLKINRVEAEDLGYYVCWOGTH-SPLTFAGTKLEIK	243	
Db	61	SGVDRFTFGSSGSDFTLKISRVEAEDGVYVCWOGTHMPPTFGQTFVEIK	113	
RESULT	3			
Q9JL85	PRELIMINARY:	PRT:	109 AA.	
AC	Q9JL85:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C;			
RA	Malkiel S., Liao L., Cunningham M.W., Diamond B.;			

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RT      "Characterization of cross-reactive monoclonal anti-mycosin/anti-n-  
RL acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
DR EMBL AF206021; AAF69319.1; --  
FT NON_TER  
SO SEQUENCE    109 AA; 11944 MM; DEF615FEECEDA4EDE CRC64;  
  
Query Match          34.4%; Score 443.5; DB 11; Length 109;  
Best Local Similarity 78.9%; Pred.No.2.6e-32;  
Matches   86; Conservative   8; Mismatches 14; Indels   1; Gaps     1  
  
QY       9 ALVSGASVKLSCTASCAGNFINKDYMHMKORPEOGLEWIGWDENGDTEAPKFGKA 68  
DB        1 ALVPGASVKSCTASCAGNIEDTYMHWKKOREGGLGNIDPATRGSKDKPKRQGA 60  
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
OY 69 TWTADTSSNTAYVLQLSLASEDTAVYYCNFYDAL-DIVGGCITYTVSS 116  
DB         61 TTSDTSSTNYTLQLSSLSEDTAVYYCVRRGAVVEDYGQGTTALTVSS 109  
           ::|||::|||||::|||::|||::|||::|||::|||::|||::|||::|||:  
  
RESULT    4  
D09ZIC4 PRELIMINARY; PRT; 118 AA.  
AC Q9ZIC4;  
DT 01-MAY-1999 (TREMBLrel. 10; Created)  
DT 01-MAY-1999 (TREMBLrel. 10; Last sequence update)  
DI 01-MAY-2000 (TREMBLrel. 13; Last annotation update)  
DE ANTI-PORCINE VCAN MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A..  
RC STRAIN-BALB/C;  
RA Mueller J.P., Glanmont M.A., Hartman S.L., Elliott E.A., Squinto S.P.,  
RM Matlis L.M., Evans W.J.;  
RT "Humanized porcine VCAN-specific monoclonal antibodies with chimeric  
RT IgG2/γ4 constant regions block human leukocyte binding to porcine  
RL endothelial cells".  
DL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.  
DR EMBL: U78801; AAC00293.1; -.  
DR INTERPRO: IPR005006; -.  
DR Pfam: PF00047; 1q; 1.  
FT NON_TER  
SQ SEQUENCE    118 AA; 13036 MM; 90DEC559D31EC4FC CRC64;  
  
Query Match          33.2%; Score 428; DB 11; Length 118;  
Best Local Similarity 71.2%; Pred.No.6.9e-31;  
Matches   84; Conservative  10; Mismatches 22; Indels   2; Gaps     1  
  
QY       1 OVOLQGSAGELVRSASYKLSCTAGSFNIKDYMVMWKORPGEGLWMGMIPENDGREX 60  
DB        1 OVOVGQSAAELARPAWSAKLKCSKAGYNFNSTMQMOKORPEGGLEMGITPPGDSITS 60  
           |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
OY 61 APRKGKTMTADTSSNTAYVLQLSLASEDTAVYYC--NFYGDALDWYGQGITTVSS 116  
DB         61 TORFKGRATLTADRKSSPAYMQLSLASSEDNAVYYCARTRGVGYDPDGWGQTTLTVSS 118  
           :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
```


FT NON_TER 1 1
 RT NON_TER 109 109
 SQ SEQUENCE 109 AA: 12118 MW: FF65E441BBF936A6 CRC64:

Query Match 29.6%; Score 381; DB 11; Length 109;
 Best Local Similarity 64.9%; Pred. No. 9.4e-27;
 Matches 72; Conservative 16; Mismatches 17; Indels 6; Gaps 2;

QY 10 ELVRSGASVRLSCTASGFNIKDYMMHWKORPEQGLEWIGMIDPENGDTETAPKPGKAT 69
 DB 1 ELVKPGASVRLSCTASGFNIKDYMMHWKORPEQGLEWIGMIDPENGDTETAPKPGKAT 60

QY 70 MTAADSSNTAYLQSLASEDTAVYYC---NFYGDALDYWGCGTIVYSS 116
 DB 61 LTSDSSSTAYVLSLTSSEDSAVYICARDGNRYG--FDYWGCGTIVYSS 109

RESULT 13
 09JUL77 PRELIMINARY; PRT: 110 AA.

AC 09JUL77: 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE ANTI-MYOSIN IMMUNOglobULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BA/2;
 RA Maltiel S., Iiao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetylglucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF206029; AAF69327.1; -
 FT NON_TER 1 1
 FT SEQUENCE 110 AA: 12138 MW: 2E2EB81FB5862C9AF CRC64;

Query Match 28.9%; Score 372; DB 11; Length 110;
 Best Local Similarity 65.8%; Pred. No. 6e-26;
 Matches 73; Conservative 11; Mismatches 19; Indels 8; Gaps 2;

QY 11 LVRSASVRLSCTASGFNIKDYMMHWKORPEQGLEWIGMIDPENGDTETAPKPGKAT 70
 DB 3 LVKPGASVRLSCTASGFNIKDYMMHWKORPEQGLEWIGMIDPENGDTETAPKPGKAT 62

QY 71 TADTSSNTAYLQSLASEDTAVYYC---NFYGDALDYWGCGTIVYSS 116
 DB 63 TVDTSSSTAYVLSLTSSEDSAVYICARDGNRYG--AMDYWGCGTIVYSS 110

RESULT 14
 09Y298 PRELIMINARY; PRT: 150 AA.

AC 09Y298: 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
 GN IGG VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98322155; PubMed=9657749;
 RA Jacquemin M.G., Vander Elst L.P.L.;

RT "Mechanism and kinetics of factor VIII inactivation: study with an
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with
 RT inhibitor."
 RL Blood 92:496-506(1998).
 DR EMBL: AJ224083; CA11829.1; -
 DR INTERPRO: IPR003006; -
 DR PFM: PF00047; 19; 1.
 DR Signal.
 FT NON_TER 1 19
 FT SEQUENCE 150 AA: 16031 MW: 563D164AB22802D5 CRC64;

Query Match 28.5%; Score 367.5; DB 4; Length 150;
 Best Local Similarity 60.7%; Pred. No. 2.2e-25;
 Matches 71; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

QY 1 QVQLQSGAEVRSASVRLSCTASGFNIKDYMMHWKORPEQGLEWIGMIDPENGDTET 60
 DB 20 QVQLVSGAEVRSASVRLSCTASGFNIKDYMMHWKORPEQGLEWIGMIDPENGDTET 79

QY 61 AKFPGKATMTADTSSNTAYLQSLASEDTAVYYCNYG-DALDYWGCGTIVYSS 116
 DB 80 AKFPGSVMTADTSSNTAYLQSLASEDTAVYYCAVPDPADFDYWGCGTIVYSS 136

RESULT 15
 09ZIC6 PRELIMINARY; PRT: 117 AA.

AC 09ZIC6: 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=BA/2;
 RA Mueller J.P., Gianmori M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Matis L.M., Evans M.J.;
 RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
 RT IgG2/4 constant regions block human leukocyte binding to porcine
 RT endothelial cells."
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U78799; AAD0291.1; -
 DR INTERPRO: IPR003006; -
 DR PFM: PF00047; 19; 1.
 FT NON_TER 1 1
 FT SEQUENCE 117 AA: 13122 MW: 4F65B193AFB77E5B CRC64;

Query Match 27.5%; Score 354.5; DB 11; Length 117;
 Best Local Similarity 58.5%; Pred. No. 2.3e-24;
 Matches 69; Conservative 15; Mismatches 31; Indels 3; Gaps 2;

QY 1 QVQLQSGAEVRSASVRLSCTASGFNIKDYMMHWKORPEQGLEWIGMIDPENGDTET 60
 DB 1 QVQLQSGAEVRSASVRLSCTASGFNIKDYMMHWKORPEQGLEWIGMIDPENGDTET 60

QY 61 AKFPGKATMTADTSSNTAYLQSLASEDTAVYYCNYGDA-IDYWGCGTIVYSS 116
 DB 61 NORLKDRLITVYDSSNTAYLQSLASEDTAVYYCT-RGEVSWFAYWGCGTIVYSS 117

Search completed: February 12, 2001, 15:24:31
 Job time: 101 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:22:45 ; Search time 28.25 seconds

(without alignments)
294.127 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289
Sequence: 1 QVQLQSGAGLVRSASVRL.....CMQGTSHPLTFGATKLEIK 243

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
A.Geneseq_36:*
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
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6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
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12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
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18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1289	100.0	243	19 W60769	Single chain antib
2	1277	99.1	535	18 W28491	Human p53 protein
3	1277	99.1	535	18 W28492	Human p53 protein
4	983.5	76.5	353	20 T06273	Anti Fc alpha rece
5	961	74.6	249	19 W60770	Single chain antib
6	911	70.7	281	20 W82744	Fusion protein PIC
7	911	70.7	270	16 W82745	Fusion protein (80
8	906	70.3	270	16 W75719	MPE-23 antibody
9	900	69.8	553	18 W15508	Single chain anti-
10	900	69.8	553	20 W32223	H22-anti-CEA anti-
11	895.5	69.5	249	9 P80154	Biosynthetic antib
12	886.5	68.8	437	19 W37738	Nucleotide sequenc

13	869	67.4	532	21 Y78328	Bispecific anti-ze
14	866	67.2	348	20 Y29910	Human IP-10 and mu
15	866	67.2	361	20 Y29912	Human MCP-3 and mu
16	863	67.0	251	20 Y17958	Mouse scFv fragmen
17	859	66.6	251	20 Y17962	Mouse scFv fragmen
18	856.5	66.4	311	11 R05378	Multi-functional pr
19	850	65.9	242	20 Y21884	Amino acid sequenc
20	848.5	65.8	311	9 Y21884	Multi-functional pr
21	843.5	65.4	288	20 W82743	Fusion protein PNG
22	843.5	65.4	289	20 Y06132	Monoclonal antibod
23	843.5	65.4	673	20 W82742	Transferrin CDW/1
24	829	64.3	248	19 W63830	H and L chain Fv r
25	828.5	64.3	247	14 R32091	H and L chain Fv r
26	828.5	64.3	248	20 Y17964	Mouse scFv fragmen
27	828.5	64.3	249	14 R32090	H and L chain Fv r
28	828.5	64.3	249	17 R95213	heavy and light ch
29	822.5	63.8	248	20 Y17960	Mouse scFv fragmen
30	816.5	63.3	305	21 Y59265	Antibody 4H5 L cha
31	816.5	63.3	305	21 Y51142	Murine derived pro
32	815.5	63.3	281	18 W27560	Consensus single c
33	813	63.1	580	20 W90217	Bispecific tetra
34	812	63.0	365	18 W35131	R. pipiens recombi
35	812	63.0	366	18 W35132	R. pipiens recombi
36	808.5	62.7	248	20 Y17965	Mouse scFv fragmen
37	808.5	62.5	253	16 R72599	Anti-dansyl single
38	804	62.4	556	20 W90218	Bispecific tetra
39	804	62.4	559	19 W37132	Anti-Tac(Fv)-PE40
40	804	62.4	599	21 Y87477	Anti-Tac(Fv)-PE40
41	803.5	62.3	249	13 R21262	pSCFVQ11 encoding
42	801.5	62.2	263	20 Y28470	Vh-(Lk)-Vl of anti
43	799	62.0	599	20 W95462	Anti-Tac(Fv)-PE40
44	798.5	61.9	260	20 W95600	Anti-digoxin scFv
45	798.5	61.9	260	20 W89101	Anti-digoxin singl

ALIGNMENTS

RESULT 1	
ID W60769	standard; Protein; 243 AA.
XX	
AC W60769;	
XX	
DT 08-SEP-1998	(first entry)
XX	
DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.	
XX	
Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;	
XX	
regulatory domain; p53 mutant; H273; W248; G281;	
KW p53-dependent trans-activating activity; restoration;	
KW tumour-suppressing activity; tumour cell; treatment;	
KW hyper-proliferation; cancer; re-stenosis; ss.	
OS Mus sp.	
XX	
PN W09818825-A1.	
XX	
PD 07-MAY-1998.	
XX	
PE 27-OCT-1997;	97WO-FR01921.
XX	
PR 29-OCT-1996;	96FR-0013176.
XX	
PA (RHON) RHONE-PCDLENC RORER SA.	
XX	
PI Debussche L, Bracco L;	
XX	
DK WPT. 1998-272140/24.	
XX	
DR N-PSDB; V36236.	
XX	
PT Restoring p53-dependent trans-activating activity to cell containing	
PT mutant p53 - by delivering single-chain antibody specific for the	

PT mutant, particularly for treatment of tumours
 XX Claim 5; Page 31; 54pp; French.
 XX
 CC The present sequence represents a single chain antibody (scFv) designated
 CC 421. The antibody binds to an epitope present in the C-terminal region
 CC of the p53 protein that includes oligomerisation and regulatory domains,
 CC specifically between positions 320 and 393. scFv 421 is directed against
 CC p53 mutants, particularly R273, W248 and G281 mutants. When the scFv is
 CC introduced into cells containing a mutant p53 protein, p53-dependent
 CC trans-activating activity is restored. scFv 421 is specific for
 CC p53-mutants that have lost tumour-suppressing activity and are present in
 CC tumour cells. It is particularly used to treat hyper-proliferation
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant
 CC and to purify or detect p53.
 XX
 SQ Sequence 243 AA:
 Query Match 100.0%; Score 1289; DB 19; Length 243;
 Best Local Similarity 100.0%; Pred. No. 2e-83;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLQSGAEIVRSASVSLCTASGFNIKDYMHVWKORPEGLMIGWIDPENGDTX 60
 DB 1 qvqlqsgaelivrsasvslctasgfnlkdymhwkqpegglwlgwidpengdtey 60
 QY 61 ARKFOGKATMTADTSSNTAYLQSLASDEPTAVYYCNFPGDALDYWGCGTTTVSSGGG 120
 DB 61 apkfkgkatmtadtsntaylqlslasdeptavyycnfygdaldywgqgtltvssggg 120
 QY 121 SGGGSGGGGSDVLMQTQPLTLSTVIGOPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180
 DB 121 sggsgsgsgsdvltmqtpiltstvtlqgpasiscsksgslldsdgktylnmllqrpqsgp 180
 QY 181 KRLLIVSKLDSGVDPDRFTGSGSGTDFTLKINRVEAEDLGVIYVCWQTHSPITFGAGTKL 240
 DB 181 krllivskldsgvdpdrftgsgsgtdftlklnrveaedlgviyvcwgthspitfgagtkl 240
 QY 241 ETK 243
 DB 241 elk 243
 RESULT 2
 ID W28491 standard; Protein: 535 AA.
 AC W28491;
 XX
 DT 25-NOV-1997 (first entry)
 DE Human p53 protein variant S-325 encoded by PBC176.
 XX
 XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
 KW substitution; replacement; transactivation; viral protein VP16; HSV;
 KW anti-oncogene; hyperproliferation; cancer; restenosis; scFv;
 KW tumour suppression; apoptosis; single chain antibody variable domain.
 XX
 XX Chimeric - Homo sapiens.
 OS Chimeric - Herpes simplex virus.
 OS Synthetic.
 XX
 PN MO9704092-A1.
 PD 06-FEB-1997.
 XX
 PF 17-JUL-1996; 96WO-FR01111.
 XX
 PR 19-JUL-1995; 95FR-0008729.
 XX
 PA (RHON ?) RHONE POULENC RORER SA.

XX Bracco L, Conseiller E;
 PI
 XX
 DR MPI: 1997-132633/12.
 XX N-PSDB: T86221.
 PT New p53 variants e.g. with oligomerisation domain replaced by
 PT leucine zipper - useful for treating hyper-proliferative disorders,
 PT esp. cancer and restenosis
 XX
 PS Claim 36; Pages 88-90; 133pp; French.
 CC
 CC Claimed variants of protein p53 have at least part of the
 CC oligomerisation domain deleted and replaced by a leucine zipper
 CC domain. The mutants preferably also have at least part of the p53
 CC transactivation domain (amino acids 1-74) deleted and replaced by
 CC the transactivating domain (TAD) from herpes simplex virus viral
 CC protein VP16 (amino acids 411-490) or by a protein domain able to
 CC bind selectively to a transactivator, especially a single-chain
 CC antibody variable domain (scFv). The present sequence is that of
 CC a specifically claimed p53 variant designated S-325 and comprising
 CC a scFv domain, amino acids 75-325 of human wild-type p53 and a
 CC leucine zipper domain at the C-terminal. The p53 variants are
 CC more active and more stable tumour suppressors and apoptosis-inducing
 CC agents than wild-type p53 and are active where the wild-type protein
 CC is not, i.e. they are not inactivated by dominant negative or oncogenic
 CC mutants, nor by other cellular proteins (because the leucine zipper
 CC domain prevents formation of inactive mixed oligomers).
 XX
 SQ Sequence 535 AA:
 Query Match 99.1%; Score 1277; DB 18; Length 535;
 Best Local Similarity 98.8%; Pred. No. 3.1e-82;
 Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QVQLQSGAEIVRSASVSLCTASGFNIKDYMHVWKORPEGLMIGWIDPENGDTX 60
 DB 3 qvqlqsgaelivrsasvslctasgfnlkdymhwkqpegglwlgwidpengdtey 62
 QY 61 ARKFOGKATMTADTSSNTAYLQSLASDEPTAVYYCNFPGDALDYWGCGTTTVSSGGG 120
 DB 61 apkfkgkatmtadtsntaylqlslasdeptavyycnfygdaldywgqgtltvssggg 122
 QY 121 SGGGSGGGGSDVLMQTQPLTLSTVIGOPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180
 DB 123 sggsgsgsgsdvltmqtpiltstvtlqgpasiscsksgslldsdgktylnmllqrpqsgp 182
 QY 181 KRLLIVSKLDSGVDPDRFTGSGSGTDFTLKINRVEAEDLGVIYVCWQTHSPITFGAGTKL 240
 DB 183 krllivskldsgvdpdrftgsgsgtdftlklnrveaedlgviyvcwgthspitfgagtkl 242
 QY 241 ETK 243
 DB 241 elk 245
 RESULT 3
 ID W28492 standard; Protein: 535 AA.
 AC W28492;
 XX
 DT 25-NOV-1997 (first entry)
 DE Human p53 protein variant S-325H.
 XX
 XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
 KW substitution; replacement; transactivation; viral protein VP16; HSV;
 KW anti-oncogene; hyperproliferation; cancer; restenosis; scFv;
 KW tumour suppression; apoptosis; single chain antibody variable domain.
 XX
 XX Chimeric - Homo sapiens.

OS	Chimeric	Herpes simplex virus.
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 361	/note= "Arg residue at position 182 of wild-type
FT		p53 has been mutated to His"
XX		
PN	W09704092-A1.	
PD		
XX	06-FEB-1997 .	
PF		
XX	17-JUL-1996; 96WO-FR01111.	
XX		
PR	19-JUL-1995; 95FR-0008729.	
XX		
PA	(RHON) RHONE POULENC RORER SA.	
XX		
PI	Bracco L, Conseiller E;	
XX		
DR	WPI; 1997-132633/12.	
XX		
PT	New p53 variants e.g. with oligomerisation domain replaced by	
PT	leucine zipper - useful for treating hyper-proliferative disorders,	
PS	esp. cancer and restenosis	
XX		
PS	Claim 36; Page -: 133pp; French.	
XX		
CC	Claimed variants of protein p53 have at least part of the	
CC	oligomerisation domain deleted and replaced by a leucine zipper	
CC	domain. The mutants preferably also have at least part of the p53	
CC	transactivation domain (amino acids 1-74) deleted and replaced by	
CC	the transactivating domain (TP) from herpes simplex virus vital	
CC	protein VP16 (amino acids 411-490) or by a protein domain able to	
CC	bind selectively to a transactivator, especially a single-chain	
CC	antibody variable domain (scFv). The present sequence is that of	
CC	a specifically claimed p53 variant designated S-325H and comprising	
CC	a scFv domain, amino acids 75-325 of human wild-type p53 (but with	
CC	Arg182 replaced by His) and a leucine zipper domain at the C-terminal.	
CC	The p53 variants are more active and more stable tumour suppressors	
CC	and apoptosis-inducing agents than wild-type p53 and are active where	
CC	the wild type protein is not, i.e. they are not inactivated by dominant	
CC	negative or oncogenic mutants, nor by other cellular proteins (because	
CC	the leucine zipper domain prevents formation of inactive mixed	
CC	oligomers).	
CC	(Note: this sequence does not appear in the specification and has	
CC	been produced by modifying the given sequence of variant V-325).	
XX		
XX	Sequence 535 AA;	

Query Match	99.1%	Score 1277:	DB 18:	Length 535:
Best Local Similarity	98.8%:	Pred. No. 3, Le 82:		
Matches 240:	Conservative 2:	Mismatches 1:	Indels 0:	Gaps 0:
QY	1	QVQLTQSGAEELVRSGASYVRLSCTASGFNRIKDYIMHWKQRPQGLEMTIGIDPENDELEY	60	
Db	3	gvdqldsgsgaelaygsasvxlctasgfnkdxlymmhwkvrppegglewslidpengdtey	62	
QY	61	APKFGKATMTADTSSNTAYLQLSLASEDDTAVYICNFTGDAIDYWGQTTVTVSSGGG	120	
Db	63	apkfsgkatmtadtsnrtaylqlslasedtavyonfygdaldywgqgtvtvssg99g	122	
QY	121	SGGGSGGGGSPVLTQMPLEPLTVYIIGQASISCKSSQSLSDDGKTYNMTLLORGGSP	180	
Db	123	sgggsgsgggspvltmqcpflrlsvltlqgpaasckssgslsdsgktynmvllqrggsp	182	
QY	181	KRLIYVSKLDSGVDRFTGSGSGTDFTLKINRVEAEDGVYVYCMQGTSPPLTFGAGTGL	240	
Db	183	krlilylsvklsgvdrftfgsgsgtdftklknrveeedglyyvcwgthsppltfagagtkl	242	
QY	241	EIK 243		

Db	243	elk	245
RESULT	4		
ID	Y06273		
XX	Y06273	standard; Protein; 353 AA.	
AC	Y06273;		
XX	23-AUG-1999	(first entry)	
DT			
XX	Anti Fc alpha receptor scFv A77-PDGR-R TM fusion.		
DE			
XX	Single chain antibody; scFv; A77; IgA receptor; Fc receptor;		
KW	Fc alpha receptor; platelet derived growth factor receptor;		
KW	antibody engineering; cell surface expression; therapy; cancer;		
RV	tumour; vaccine; human.		
XX			
OS	Chimeric - Mus sp.		
OS	Chimeric - synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Domain	1..21	
FT		/note="Ig K-chain SP"	
FT	Peptide	22..30	
FT		/note="HA epitope"	
FT	Domain	38..160	
FT		/note="A77 VL"	
FT	Peptide	161..175	
FT		/note="linker"	
FT	Domain	176..287	
FT		/note="A77 VH"	
FT	Peptide	294..303	
FT		/note="Myc epitope"	
FT	Domain	304..353	
FT		/note="PDGFR transmembrane domain"	
XX			
XX	WO9928349-A2.		
PN	10-JUN-1999.		
PD			
XX	02-DEC-1998; 98WO-US25556.		
XX			
XX	02-DEC-1997; 97US-0067232.		
PR			
PA	(MEDA-) MEDAREX INC.		
XX			
XX			
PI	Deo YM, Goldstein J, Graziano R, Keller T;		
XX			
DR	WPI; 1999-371099/21.		
DR	N-PSDB; X58936.		
XX			
PT	Cells expressing anti-Fc receptor binding components		
XX			
PS	Example 6; Fig 10A-E; 68pp; English.		
XX			
CC	The present sequence represents a fusion protein comprising murine		
CC	anti-Fc alpha receptor antibody A77 sfv and the transmembrane domain		
CC	of platelet derived growth factor receptor (PDGFR-R TM). It is		
CC	encoded by expression vector pUG718 (see X58935). Murine tumour		
CC	cells transformed to express A77-TM were able to bind a soluble form		
CC	of the Fc alpha receptor, and the bound receptor was able to engage		
CC	IgA molecules. This is an example of cells of the invention that		
CC	have been transformed to express on their surface a component which		
CC	binds to an Fc receptor of an effector cell. The transformed cell		
CC	is targeted to an effector cell via the Fc binding component, and		
CC	can be used as a vehicle to increase an effector cell-mediated		
CC	immune response, such as cell lysis and phagocytosis, against an		
CC	antigen associated with the cell. The transformed cells are used		
CC	to treat cancer and infectious diseases or used as vaccines. The		
CC	method allows for killing of target cells without targeting any		
CC	particular antigen on the cell. This is advantageous since many		
CC	tumour cells and other target cells do not have defined antigens		

FT	Region	76..85
FT	/note="CDR H2"	
FT	Region	86..124
FT	/note="FR H3"	
FT	Region	125..135
FT	/note="CDR H3"	
FT	Region	136..146
FT	/note="FR H4"	
FT	Peptide	147..161
FT	/note="linker"	
FT	Region	162..184
FT	/note="FR L1"	
FT	Region	185..194
FT	/note="CDR L1"	
FT	Region	195..209
FT	/note="FR L2"	
FT	Region	210..216
FT	/note="CDR L2"	
FT	Region	217..248
FT	/note="FR L3"	
FT	Region	249..257
FT	/note="CDR L3"	
FT	Region	258..267
FT	/note="FR L4"	
XX		
PN	W09515341-A1.	
PD	08-JUN-1995.	
XX		
PF	05-DEC-1994;	94WO-GB02658.
XX		
PR	03-DEC-1993;	93GB-0024807.
PA	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.	
XX		
PI	Begent RHJ, Chester KA, Hawkins RE;	
XX		
DR	WPI; 1995-215234/28.	
DR	N-PSDB; Q90663.	
XX		
PT	Antibody for carcinoembryonic antigen - for treatment and diagnosis	
PT	of colorectal cancer	
XX		
PS	Claim 3; Page 48-49; 72pp; English.	
XX		
CC	This sequence represents the MFE-23 antibody, which is an antibody	
CC	against carcinoembryonic antigen (CEA). CEA is a marker antigen for	
CC	cancer imaging and therapy. The MFE-23 antibody sequence was obtained	
CC	using phage technology. In this process, mice were immunised with CEA.	
CC	The antibody variable region genes obtained from these mice were then	
CC	amplified from cDNA and cloned as a single chain Fv (scFv) into	
CC	bacteriophage vectors, producing a library. The phages that bound to	
CC	biotinylated CEA were selected and amplified, and this sequence (and the	
CC	encoding cDNA) were selected. This sequence was found to have good	
CC	specificity and affinity for CEA, meaning that it can be used in targeted	
CC	anti-tumour therapies. A humanised antibody with the complementarity	
CC	determining regions of MFE-23 may be produced by CDR grafting. The	
CC	antibody may be used for the treatment by surgery or therapy of a	
CC	colorectal tumour, or in the diagnosis of a colorectal tumour. MFE-23	
CC	may also be used to make diabodies (bivalent or bispecific antibody	
CC	fragments which bind to two different antigens), and may be linked to an	
XX	antitumour agent or a detectable label.	
XX		
Sequence	270 AA;	

```

Query Match      70.3%   Score 906   DB 16   length 270;
Best Local Similarity 69.2%   Pred No. 1.5e-56;
Matches 173; Conservative 26; Mismatches 33; Indels 16; Gaps 3
0Y 1 QVQLQSGAEIYVNGSAVSKTCTASGFNITKIDYMEWKVQRPQGLTIGWIDPENGDTREY 60
   |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
27 q'r'k'q'g's'a'e'l'v's'g't's'v'k'e'a's'i'n'l'k'd's'm'h'l'r'i'p'e'q'g'l'e'w'i'g'v'd'p'e'n'g'd'e'y 86

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QY 61 AFRQGRKAIWADHDSNMTAYIOLASLSEDPAYVYKC-----FYGDADLYMCOQGTVE 113
Db 87 aqkfqgacrfctcdsntaylqslscsdtaayycneqreptgpyr---fdywgqctvc 143
QY 114 VSSGGGSGGGSGGGSGGSDVLMTOTPLTLVTTIGOPASISCKSSQSLDSDGKTYLNMML 173
Db 144 vssggsgsgsgsgsgsgsenvlltqpslmaaspekvcticsaasyr-----symhwfq 197
QY 174 QRPGQSRRLTYLVSKLDSGVPDPEFTSGSGSTDPDTLAINVLEADDLVYICMGGTHSPLT 233
Db 198 qkqpspsmawysstslnaasvparfssgsgstysylstlsmeeadaaelyccqqrssypl 257
QY 234 FGAGTKLEIK 243
Db 258 fgaagtkleik 267

```

RESULT	9	
ID	W11508	
AC	W11508 standard: Protein; 553 AA.	
XX	W11508;	
DT	24-SEP-1997 (first entry)	
XX		
DE	Single chain anti-Fc gamma RI antibody fused to anti-CEA antibody.	
XX		
XX	Humanised antibody; anti-Fc receptor; H22, bifunctional; dispecific;	
KM	fusion protein; chimera; carcinoembryonic antigen; CEA.	
XX		
OS	Chimeric - Mus musculus.	
OS	Chimeric - Homo sapiens.	
OS	Synthetic.	
XX		
Key	Location/Qualifiers	
FT	1..19	
FT	/label= signal_peptide	
FT	20..139	
FT	/label= H22_VH	
FT	/note= "anti-Fc gamma RI antibody H22 heavy chain variable domain"	
FT	140..154	
FT	/label= linker	
FT	155..266	
FT	/label= H22_VL	
FT	/note= "anti-Fc gamma RI antibody H22 light chain variable domain"	
FT	267..276	
FT	/label= linker	
FT	277..396	
FT	/label= MFE-23_VH	
FT	/note= "anti-CEA antibody MFE-23 heavy chain variable domain"	
FT	397..411	
FT	/label= linker	
FT	412..520	
FT	/label= MFE-23_VL	
FT	/note= "anti-CEA antibody MFE-23 light chain variable domain"	
FT	521..533	
FT	/label= linker	
FT	534..544	
FT	/label= c-myc_tag	
FT	548..553	
FT	/label= His-6_tail	
FT	/note= "6 histidine residues"	
XX		
XX	MO9646789-AI.	
XX		
XX	19-DEC-1996.	
XX		
XX	07-JUN-1996.	
XX	66WO-US09988.	

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XX 07-JUN-1995; 95US-0484172.
PR (MEDA-) MEDAREX INC.
XX Deo YM, Goldstein J, Graziano R, Somasundaram C;
XX WPI: 1997-052242/05.
DR N-PSDB: T58130.
XX
XX Recombinant, multi-specific anti-Fc receptor antibody molecules
XX also comprise an anti-target portion, used for the treatment of
XX cancer, autoimmune disease and pathogenic infection
XX
XX Example 8; Fig 40; 115pp; English.
XX
XX A mammalian expression construct encoding a single chain antibody
XX having binding specificity for Fc gamma RI, derived from the
XX humanised anti-Fc gamma RI monoclonal antibody H22 was prepared
XX (see T58129). A bispecific single chain polypeptide was produced
XX by fusing the H22 scfv to an anti-carcinoembryonic antigen (CEA)
XX antibody. The H22-anti-CEA fusion protein was shown to bind both
XX Fc gamma RI and CEA.
XX
XX Sequence 553 AA:
SQ
XX
XX Query Match 69.8%; Score 900; DB 18; Length 553;
XX Best Local Similarity 68.7%; Pred. No. 8e-56;
XX Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;
XX
XX 2 VOLOSGAELVRSAGSVKLSCTASGFNINQDYMHVYKORPEGLWIGWIDPENGDETEYA 61
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX Db 278 IklqgsgeaelvrsqgsvklsctasgfniKdsymhwlrgpgeglwlgwidpengdteya 337
XX
XX 62 PKFGKATMTADTSSNTAYLQSLASLSEDTAVYYCN-----FYGDALDYWGCGTTVV 114
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX Db 338 pkfgkattfddtsntaylqlsltsedlavycneqptgpyy---fdyvgggttivr 394
XX
XX 115 SSGGGSGGGSGGGSDVLMQTPLTSLVTIGQPASISCKSSQLSDSGKTYLNMILQ 174
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX Db 395 ss9sgsgsgsgsgseavlqspalmsaspgekyltlcsassv-----symhwfqq 448
XX
XX 175 RFGQSPKRLIYVSKLDSGVDPDRFTGSGSGTDFTLKINRVEADLGVYICWOGTSPLEF 234
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX Db 449 kpgtspkrlwystcslasvparfsgsgstysltlsmeeadaatytcqgrsspylft 508
XX
XX 235 GAGTKLEIK 243
XX ::::::::::::::
XX Db 509 gagtkleik 517
XX
XX RESULT 10
XX W73223
XX ID W73223 standard; Protein; 553 AA.
XX
XX AC W73223;
XX
XX DT 25-JAN-1999 (first entry)
XX
XX DE H22-anti-CEA antibody construct 321.
XX
XX KM Multispecific single chain antibody; antibody H22; tumour cell; therapy;
XX antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;
XX epidermal growth factor receptor; breast cancer; ovarian cancer.
XX
XX OS Synthetic.
XX
XX PN US5837243-A.
XX
XX PD 17-NOV-1998.
XX
XX PF 07-JUN-1996; 96US-0661052.

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XX 07-JUN-1996; 96US-0661052.
PR 07-JUN-1995; 95US-0484172.
XX (MEDA-) MEDAREX INC.
XX Deo YM, Goldstein J, Graziano R, Somasundaram C;
XX WPI: 1999-023374/02.
DR N-PSDB: V08176.
XX
XX Specific killing of tumour cells - using a multi-specific molecule
XX comprising an anti-Fc receptor antibody and a portion which binds to
XX a target cell
XX
XX Example 8; Fig 40; 57pp; English.
XX
XX This sequence represents the construct 321, which is a fusion between an
XX anti-CEA antibody and a multispecific single chain antibody designated
XX H22. The antibody can be used in the method of the invention for inducing
XX antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell
XX which is characterised by overexpression of HER 2/neu or epidermal growth
XX factor receptor (EGFR), comprises contacting the tumour cell with a
XX multispecific protein molecule (preferably a single chain antibody)
XX comprising: (a) an anti-Fc receptor antibody or an antigen binding
XX fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which
XX binds to EGFR. The method can be used for treating cancers especially
XX breast cancer or ovarian cancer. The multispecific antibody can also
XX be administered prophylactically to vaccinate a subject against infection
XX by a target cell.
XX
XX Sequence 553 AA:
SQ
XX
XX Query Match 69.8%; Score 900; DB 20; Length 553;
XX Best Local Similarity 68.7%; Pred. No. 8e-56;
XX Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;
XX
XX 2 VOLOSGAELVRSAGSVKLSCTASGFNINQDYMHVYKORPEGLWIGWIDPENGDETEYA 61
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX Db 278 IklqgsgeaelvrsqgsvklsctasgfniKdsymhwlrgpgeglwlgwidpengdteya 337
XX
XX 62 PKFGKATMTADTSSNTAYLQSLASLSEDTAVYYCN-----FYGDALDYWGCGTTVV 114
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX Db 338 pkfgkattfddtsntaylqlsltsedlavycneqptgpyy---fdyvgggttivr 394
XX
XX 115 SSGGGSGGGSGGGSDVLMQTPLTSLVTIGQPASISCKSSQLSDSGKTYLNMILQ 174
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX Db 395 ss9sgsgsgsgsgseavlqspalmsaspgekyltlcsassv-----symhwfqq 448
XX
XX 175 RFGQSPKRLIYVSKLDSGVDPDRFTGSGSGTDFTLKINRVEADLGVYICWOGTSPLEF 234
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
XX Db 449 kpgtspkrlwystcslasvparfsgsgstysltlsmeeadaatytcqgrsspylft 508
XX
XX 235 GAGTKLEIK 243
XX ::::::::::::::
XX Db 509 gagtkleik 517
XX
XX RESULT 11
XX P80154
XX ID P80154 standard; protein; 249 AA.
XX
XX AC P80154;
XX
XX DT 01-JAN-1980 (first entry)
XX
XX DE Biosynthetic antibody binding site.
XX
XX KM Biosynthetic antibody binding site; framework region; assay; imaging;
XX multifunctional protein.
XX
XX PN W08809344-A.

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XX 01-DEC-1988.
PD 19-MAY-1988; 88WO-US01737.
XX PF 21-MAY-1987; 87US-0052800.
XX PR (CREA-) CREATIVE BIOMOLECULES INC.
XX PA Huston JS, Oppermann H;
XX PI WPI: 1988-353928/49.
XX DR N-PSDB; N80180.
XX
XX Recombinant multifunctional protein - having antibody binding site and a
PT sequence for biological activity, ion sequestering or binding to a
PT solid support.
PS Disclosure; 15pp; English.
XX
XX The biosynthetic antibody binding site forms part of a recombinant
CC multifunctional protein which also comprises an effector protein, an AA
CC acid sequence capable of sequestering an ion, or a sequence capable of
CC binding to a solid support. The BABS comprises the framework region from
CC murine anti-digoxin monoclonal antibody 26-10-heavy chain variable region
CC and the complementarily determining region from G-loop-4 heavy chain
CC variable region and has lysozyme specificity. The effector protein is an
CC enzyme, toxin, receptor, binding site, growth factor, cytokine
CC or antimetabolite. The sequence capable of sequestering an ion is
CC calmodulin or metallothionein. The sequence capable of binding to solid
CC support is streptavidin or a protein A fragment. The protein may be used
CC for, eg specific binding assays, affinity purification, biocatalysts, drug
CC targeting, imaging and immunological treatment of oncogenic etc.
CC diseases. The protein offers fewer cleavage sites to circulating
CC proteolytic enzymes and have improved stability. They reach target organs
CC rapidly and are cleared quickly from the body. They also have reduced
CC immunogenicity.
XX
XX Sequence 249 AA:
SQ
Query Match 69.5%; Score 895.5; DB 9; Length 249;
Best Local Similarity 67.8%; Pred. No. 7.3e-56;
Matches 167; Conservative 35; Mismatches 38; Indels 7; Gaps 2;
```

```
XX Nucleotide sequence encoding the Mgr6-clavin immunotoxin.
DE Recombinant ribosomal inhibitor protein; RIP; clavin; inhibition.
XX protein synthesis; conjugate; Mgr6-clavin; anticancer; antiviral agent.
XX KM Chimeric - Aspergillus clavatus.
XX OS Chimeric - Mus musculus
XX
XX Key Location/Qualifiers
FH Peptide 96..286
FT /note="Mgr6 from M. musculus"
FT Peptide 287..437
FT /note="Clavin from A. clavatus"
XX
XX WO9749726-A1,
XX
XX 31-DEC-1997.
XX
XX 26-JUN-1997; 97WO-EP03359.
XX
XX 27-JUN-1996; 96IT-FI00155.
XX
XX (ITVY-) ITAL MIN UNIV RICERCA SCI e TECNOLOGICA.
XX Colnaghi M, De Santis R, Mele A, Parente D;
XX
XX WPI: 1998-077109/07.
XX N-PSDB; V09256.
XX
XX DNA encoding Aspergillus clavatus-derived ribosomal inhibitor
PT protein, clavin - useful as an immuno-conjugate and for treatment of
PT cancer
XX
XX Claim 4; pages 14-15; 26pp; English.
XX
XX This is the amino acid sequence of a fusion protein comprising of the
CC Mgr6 single chain antibody (with the heavy and light chain joined by
CC a linker), fused to the clavin protein. Clavin is an inhibitor
CC protein, and functions by inactivating the ribosomes. Clavin or its
CC conjugates are useful as anticancer and/or antiviral agents. The
CC recombinant ribosomal inhibitor protein (RIP), Mgr6-clavin (a conjugate
CC of clavin) is used as an immunoconjugate, and the complex and clavin
CC alone are capable of inhibiting ribosomal activity.
XX
XX Sequence 437 AA:
SQ
Query Match 68.8%; Score 886.5; DB 19; Length 437;
Best Local Similarity 70.2%; Pred. No. 5.6e-55;
Matches 172; Conservative 26; Mismatches 44; Indels 3; Gaps 2;
```


RESULT 13
ID Y78328 standard; Protein: 532 AA.
XX Y78328;
AC Y78328;
XX 04-MAY-2000 (first entry)
XX Bispecific anti-zeta-chain/anti-EpCAM antibody protein sequence.
DE Anti-zeta-chain antibody 2-B-5; rat; human zeta chain; immunisation;
XX complementary determining region; CDR; autoimmune disease; cytostatic;
KW immune deficiency; T-cell malignancy; infectious disease; antiviral;
XX immunosuppressive; antimicrobial; immune response modulator; NK-cell.
OS Rattus norvegicus.
XX Synthetic.
XX WO200003016-A1.
XX 20-JAN-2000.
XX 09-JUL-1999; 99WO-EP04838.
XX 10-JUL-1998; 98EP-0112867.
XX (CONN-) CONNEX GMBH.
XX Retler C;
XX WPI: 2000-160926/14.
DR N-PSDB: 288358.
XX New oligonucleotide, polypeptide, antibody useful for treating
PT autoimmune disease, immune deficiencies, T-cell malignancies and
XX infectious diseases -
XX Example 9; Page 74-76; 79pp; English.
XX
XX The present invention describes a nucleic acid molecule (1) encoding at
CC least one complementary determining region (CDR) of a variable region of
CC an antibody which specifically interacts with the extracellular domain of
CC the human zeta-chain. The antibody whose CDR of a variable region is
CC encoded by (1), is obtained by immunising a rat with jurkat cells and
CC subsequently with a conjugate comprising a carrier molecule and a
CC anti-zeta-chain antibody is useful for the treatment and prevention of
CC autoimmune diseases, immune deficiencies, T-cell malignancies,
CC infectious diseases, and the suppression of immune response preferably in
CC order to avoid graft rejection after organ transplantation, malignancies,
CC or viral infections. The antibody, and fragments of it, can be useful for
CC the enhancement or suppression of NK-cell dependent immunity or for the
CC treatment of NK-cell derived malignancies. It can also be useful for the
CC determination of zeta-chain or eta-chain expression on NK-cells,
CC T-lymphocytes or their precursors. The present sequence represents a
CC bispecific anti-zeta-chain/anti-EpCAM antibody, from an example from
CC the present invention.
XX
XX Sequence 532 AA:
SQ

Query Match 67.4%; Score 869; DB 21; Length 532;
Best Local Similarity 47.2%; Pred. No. 1,1e-53;
Matches 1/9; Conservative 27; Mismatches 37; Indels 136; Gaps 2;

QY 1 OVOLQSGALVRSVSKLSTASGFNINIKYIMHWKQRFEGLEWIGWIDPENGDTX 60
DB 142 qvqlqgsgeelvpvgsavkskasyftfsymhwhkqpgnglewlgvlypgngntky 201
QY 61 APFQKATMTATSSNTATVLOSLASEDTANYIC----- 96
DB 202 nqfngkatltadkssstasmjstsedasavfcardwhysyylrpfaywgggtlvt 261

QY 97 ----- 96
DB 262 vssgsgsevjllqsgaelpargasvklscasgytftnyglswkqrpqgvlwlgv 321
QY 97 -----NFYGD-----LD 104
DB 322 yprlgnaynekfkqkatltadkssstasmelrsltsedasyfcarigsydlndwyfd 381
QY 105 YWGGGTTVTVSSGGSGSGSDVLMQFPLTLSTVIGOPASISCKSSQSLIUSD 164
DB 382 vwgqgtvtvssgsgsgsgsgselvmcqpclslpvslygdqaslsrsgslvshn 441
QY 165 GRTYINMLQRFQSGSEKRLIVVSKLDSGVPDRFTGSGSGIDFTKINVEAEDGVYIC 224
DB 442 gntylhwylyhkgpgsklllykvsntfsgpdrfsgsgsgtdftklisrveadlgyfc 501
QY 225 WQGHSPPLTFGAGTKLEIK 243
DB 502 sgsthyvylfsgggtkllek 520

RESULT 14
ID Y29910 standard; Protein: 348 AA.
XX Y29910;
AC Y29910;
XX 17-NOV-1999 (first entry)
XX Human IP-10 and murine scFv20A fusion protein.
XX Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX Homo sapiens.
OS Mus sp.
XX Synthetic.
XX WO9946392-A1.
XX 16-SEP-1999.
XX 12-MAR-1999; 99WO-US05345.
XX 12-MAR-1998; 98US-0077745.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Kwak LW, Biragyn A;
XX WPI: 1999-551418/46.
XX New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX Disclosure: Page 114-115; 142pp; English.
XX
XX The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocytic chemotactic protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.

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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:22:50 ; Search time 76.8 seconds

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Title: US-09-297-181-2

Perfect score: 1289

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1289	100.0	243	US-09-297-181-2	Sequence 2, Appli
2	1277	99.1	535	US-08-983-035-38	Sequence 38, Appl
3	970.5	75.3	257	US-09-419-788-113	Sequence 113, Appl
4	961	74.6	249	US-09-297-181-4	Sequence 4, Appli
5	930.5	72.2	238	US-09-559-019-28	Sequence 28, Appl

6	926.5	71.9	240	19	US-09-559-019-27	Sequence 27, Appl
7	902	70.0	251	1	PCT-US00-19843-11	Sequence 11, Appl
8	900.5	69.9	271	27	US-09-523-095A-30	Sequence 30, Appl
9	900.5	69.9	274	27	US-09-523-095A-26	Sequence 26, Appl
10	900	69.8	553	17	US-09-364-088-16	Sequence 16, Appl
11	900	69.8	553	19	US-09-523-279-16	Sequence 16, Appl
12	900	69.8	553	27	US-09-188-082-16	Sequence 16, Appl
13	892.5	69.2	245	27	US-09-523-095A-40	Sequence 40, Appl
14	892.5	69.2	271	27	US-09-523-095A-34	Sequence 34, Appl
15	892.5	69.2	274	27	US-09-523-095A-32	Sequence 32, Appl
16	891	69.1	251	1	PCT-US00-19843-15	Sequence 15, Appl
17	891	69.1	264	1	PCT-US00-19843-8	Sequence 8, Appl
18	875.5	67.9	267	18	US-09-419-788-30	Sequence 30, Appl
19	866	67.2	348	20	US-09-646-028-12	Sequence 12, Appl
20	866	67.2	361	20	US-09-646-028-14	Sequence 14, Appl
21	854.5	66.3	242	19	US-09-594-985A-5	Sequence 5, Appl
22	850	65.9	242	16	US-09-202-000-14	Sequence 14, Appl
23	834	64.7	271	19	US-09-594-985A-6	Sequence 6, Appl
24	833.5	64.7	272	19	US-09-594-985A-7	Sequence 7, Appl
25	832	64.5	262	19	US-09-594-985A-4	Sequence 4, Appl
26	829	64.3	248	13	US-08-996-140-23	Sequence 23, Appl
27	828.5	64.3	247	7	US-08-331-396C-34	Sequence 34, Appl
28	828.5	64.3	247	7	US-08-331-396A-34	Sequence 34, Appl
29	828.5	64.3	247	7	US-08-331-397-34	Sequence 34, Appl
30	828.5	64.3	247	7	US-08-331-398-34	Sequence 34, Appl
31	828.5	64.3	247	11	US-08-759-804-34	Sequence 34, Appl
32	828.5	64.3	247	16	US-09-227-693-34	Sequence 34, Appl
33	828.5	64.3	248	7	US-08-331-396C-34	Sequence 34, Appl
34	828.5	64.3	248	7	US-08-331-396D-34	Sequence 34, Appl
35	815.5	63.3	281	14	US-09-025-769B-178	Sequence 178, App
36	813	63.1	580	18	US-09-468-029-58	Sequence 58, Appl
37	809.5	62.8	269	14	US-09-070-408-132	Sequence 132, App
38	809.5	62.8	269	22	US-06-045-409-132	Sequence 132, App
39	805.5	62.5	253	1	PCT-US94-11411-6	Sequence 6, Appl
40	805.5	62.5	253	5	US-08-134-536-6	Sequence 6, Appl
41	805.5	62.5	253	8	US-08-440-764-6	Sequence 6, Appl
42	805.5	62.5	253	12	US-08-838-521-6	Sequence 6, Appl
43	804	62.4	556	18	US-09-468-029-60	Sequence 60, Appl
44	801.5	62.2	263	16	US-09-293-533-66	Sequence 66, Appl
45	799	62.0	239	18	US-09-431-213-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-297-181-2
; Sequence 2, Application US/09297181
; GENERAL INFORMATION:
; APPLICANT: Bracco, Laurent
; APPLICANT: Debussche, Laurent
; TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES
; FILE REFERENCE: S196030-US
; CURRENT APPLICATION NUMBER: US/09/297,181
; CURRENT FILING DATE: 1999-04-26
; EARLIER APPLICATION NUMBER: PCT/FR97/01921
; EARLIER FILING DATE: 1997-10-27
; EARLIER APPLICATION NUMBER: FR96/13176
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentia Ver. 2.0
; SEQ ID NO 2:
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-297-181-2

Query Match 100.0%; Score 1289; DB 16; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.3e+102;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVLOQSGAEIVRSGASVYLSTASGFNIKDYMHVWVKRPEGLRWIGWIPENDTEY 60

Db 1 OVOLOSGAELVSGASVSKLSTCTASGFNIDKYMHVWKORPEOGLWIGMIDPENGDTXY 60
QY 61 APFGKATMTADTSSNTAYLQLSLASEDTAVYCNFYGDALDYGOGTTVSSGGG 120
Db 61 APFGKATMTADTSSNTAYLQLSLASEDTAVYCNFYGDALDYGOGTTVSSGGG 120
QY 121 SGGGSGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180
Db 121 SGGGSGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180
QY 181 KRILYVSKLSDGVPDRFTGSGGDTFTLKINRVEADLGVYCNQGTSPPLTFGAGTKL 240
Db 181 KRILYVSKLSDGVPDRFTGSGGDTFTLKINRVEADLGVYCNQGTSPPLTFGAGTKL 240
QY 241 EIK 243
Db 241 EIK 243

RESULT 2

US-08-983-035-38
Sequence 38, Application US/08983035
GENERAL INFORMATION:
APPLICANT: CONSEILLER, Emmanuel
APPLICANT: BRACCO, Laurent
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Maitstop 3043
CITY: Colleegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,035
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: FR 95/08729
APPLICATION NUMBER: 19-JUL-1995
FILING DATE: 19-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR96/01111
FILING DATE: 17-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95044-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ. ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-983-035-38

Query Match 99.1%; Score 1277; DB 13; Length 535;
Best local Similarity 98.8%; Pred. No. 3,6e-101;
Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY OVOLOSGAELVSGASVSKLSTCTASGFNIDKYMHVWKORPEOGLWIGMIDPENGDTXY 60
|||||

Db 3 OVOLOSGAELVSGASVSKLSTCTASGFNIDKYMHVWKORPEOGLWIGMIDPENGDTXY 62
QY 61 APFGKATMTADTSSNTAYLQLSLASEDTAVYCNFYGDALDYGOGTTVSSGGG 120
Db 61 APFGKATMTADTSSNTAYLQLSLASEDTAVYCNFYGDALDYGOGTTVSSGGG 122
QY 121 SGGGSGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180
Db 121 SGGGSGGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 182
QY 181 KRILYVSKLSDGVPDRFTGSGGDTFTLKINRVEADLGVYCNQGTSPPLTFGAGTKL 240
Db 181 KRILYVSKLSDGVPDRFTGSGGDTFTLKINRVEADLGVYCNQGTSPPLTFGAGTKL 242
QY 241 EIK 243
Db 241 EIK 243

RESULT 3

US-09-419-788-113
Sequence 113, Application US/09419788
GENERAL INFORMATION:
APPLICANT: FISCHER, Rainer
APPLICANT: SCHILLBERG, Stefan
APPLICANT: NAHRING, Jorg
APPLICANT: SACK, Markus
APPLICANT: MONECKE, Michael
APPLICANT: LIAO, Yu-Cal
APPLICANT: SPIEGEL, Holger
APPLICANT: ZIMMERMAN, Sabine
APPLICANT: EMANS, Neil
TITLE OF INVENTION: Molecular Pathogenicicidie Mediated Plant Disease
TITLE OF INVENTION: Resistance
FILE REFERENCE: 0147-0189P
CURRENT APPLICATION NUMBER: US/09/419,788
CURRENT FILING DATE: 1999-10-18
EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER FILING DATE: 1998-10-16
EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
NUMBER OF SEQ. ID NOS: 163
SOFTWARE: Patentin Ver. 2.1
SEQ. ID NO 113
LENGTH: 257
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
US-09-419-788-113

Query Match 75.3%; Score 970.5; DB 18; Length 257;
Best local Similarity 77.2%; Pred. No. 2,8e-75;
Matches 193; Conservative 13; Mismatches 33; Indels 11; Gaps 3;

QY 1 OVOLOSGAELVSGASVSKLSTCTASGFNIDKYMHVWKORPEOGLWIGMIDPENGDTXY 60
Db 3 EVOLOSGAELVSGASVSKLSTCTASGFNIDKYMHVWKORPEOGLWIGMIDPENGDTXY 62
QY 61 APFGKATMTADTSSNTAYLQLSLASEDTAVYCNFYGDALDYGOGTTVSSGGG- 119
Db 61 APFGKATMTADTSSNTAYLQLSLASEDTAVYCNFYGDALDYGOGTTVSSGGG- 118
QY 120 --GSG--GSGSGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLL 173
Db 120 --GSG--GSGSGGGSDVLMOTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNMLL 178
QY 174 QRPQSPKRLIYVSKLSDGVPDRFTGSGGSDTFTLKINRVEADLGVYCNQGTSPPLT 233
Db 174 QRPQSPKRLIYVSKLSDGVPDRFTGSGGSDTFTLKINRVEADLGVYCNQGTSPPLT 238

QY 234 FGAGTKLEIK 243
|||
Db 239 FGAGTKLEIK 248

RESULT 4
US-09-297-181-4
; Sequence 4, Application US/09297181
; GENERAL INFORMATION:
; APPLICANT: Bracco, Laurent
; APPLICANT: Debussche, Laurent
; TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES
; FILE REFERENCE: ST96030-US
; CURRENT APPLICATION NUMBER: US/09/297,181
; EARLIER FILING DATE: 1999-04-26
; EARLIER APPLICATION NUMBER: PCT/FR97/01921
; EARLIER FILING DATE: 1997-10-27
; EARLIER APPLICATION NUMBER: FR96/13176
; EARLIER FILING DATE: 1996-10-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-297-181-4

Query Match 74.6%; Score 961; DB 16; Length 249;
Best Local Similarity 74.8%; Pred. No. 1.7e-74;
Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;

QY 1 OVLOOQSGAEIVRSASVRLSCTASGFNIDYMHVVKORPEGLMIGMIDPENGDTEY 60
|||
Db 1 OVLOOQSGAEIVRSASVRLSCTASGFNIDYMHVVKORPEGLMIGMIDPENGDTEY 60
QY 61 APRFOGKATMTADTSSNTAYLQLSLASEDTAVYYCN-----FYGDALDYWGCGTIVY 114
|||
Db 61 APRFOGKATMTADTSSNTAYLQLSLASEDTAVYYCN-----FYGDALDYWGCGTIVY 114
QY 115 GSGGGGSGGGGSDVMTOTPLTLVTTIGOPASISCKSSQSLDSDGKTYLNMLLORPGOS 173
|||
Db 121 GSGGGGSGGGGSDVMTOTPLTLVTTIGOPASISCKSSQSLDSDGKTYLNMLLORPGOS 173
QY 174 ORGQSPKRLIVKLSGVPDRFTGSGGSDTFLKINRYAEADLGYVCMQGHSPLEFGAGTK 233
|||
Db 181 ORGQSPKRLIVKLSGVPDRFTGSGGSDTFLKINRYAEADLGYVCMQGHSPLEFGAGTK 233
QY 234 FGAGTKLEIK 243
|||
Db 240 FGAGTKLEIK 249

RESULT 5
US-09-559-019-28
; Sequence 28, Application US/09559019
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: Sequence Listings 1-34 for 381-71
; CURRENT APPLICATION NUMBER: US/09/559,019
; CURRENT FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
US-09-559-019-28

Query Match 72.2%; Score 930.5; DB 19; Length 238;

Best Local Similarity 71.7%; Pred. No. 6.8e-72;
Matches 175; Conservative 27; Mismatches 35; Indels 7; Gaps 2;

QY 1 OVLOOQSGAEIVRSASVRLSCTASGFNIDYMHVVKORPEGLMIGMIDPENGDTEY 60
|||
Db 1 OVLOOQSGAEIVRSASVRLSCTASGFNIDYMHVVKORPEGLMIGMIDPENGDTEY 60
QY 61 APRFOGKATMTADTSSNTAYLQLSLASEDTAVYYCN-----FYGDALDYWGCGTIVY 119
|||
Db 61 APRFOGKATMTADTSSNTAYLQLSLASEDTAVYYCN-----FYGDALDYWGCGTIVY 119
QY 120 GSGGGGSGGGGSDVMTOTPLTLVTTIGOPASISCKSSQSLDSDGKTYLNMLLORPGOS 179
|||
Db 121 GSGGGGSGGGGSDVMTOTPLTLVTTIGOPASISCKSSQSLDSDGKTYLNMLLORPGOS 179
QY 180 PKRLIVKLSGVPDRFTGSGGSDTFLKINRYAEADLGYVCMQGHSPLEFGAGTK 239
|||
Db 175 PKRLIVKLSGVPDRFTGSGGSDTFLKINRYAEADLGYVCMQGHSPLEFGAGTK 239
QY 240 LEIK 243
|||
Db 235 LEIK 238

RESULT 6
US-09-559-019-27
; Sequence 27, Application US/09559019
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: Sequence Listings 1-34 for 381-71
; CURRENT APPLICATION NUMBER: US/09/559,019
; CURRENT FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse
US-09-559-019-27

Query Match 71.9%; Score 926.5; DB 19; Length 240;
Best Local Similarity 71.7%; Pred. No. 1.5e-71;
Matches 175; Conservative 26; Mismatches 36; Indels 7; Gaps 2;

QY 1 OVLOOQSGAEIVRSASVRLSCTASGFNIDYMHVVKORPEGLMIGMIDPENGDTEY 60
|||
Db 1 OVLOOQSGAEIVRSASVRLSCTASGFNIDYMHVVKORPEGLMIGMIDPENGDTEY 60
QY 61 APRFOGKATMTADTSSNTAYLQLSLASEDTAVYYCN-----FYGDALDYWGCGTIVY 119
|||
Db 61 APRFOGKATMTADTSSNTAYLQLSLASEDTAVYYCN-----FYGDALDYWGCGTIVY 119
QY 120 GSGGGGSGGGGSDVMTOTPLTLVTTIGOPASISCKSSQSLDSDGKTYLNMLLORPGOS 179
|||
Db 121 GSGGGGSGGGGSDVMTOTPLTLVTTIGOPASISCKSSQSLDSDGKTYLNMLLORPGOS 179
QY 180 PKRLIVKLSGVPDRFTGSGGSDTFLKINRYAEADLGYVCMQGHSPLEFGAGTK 239
|||
Db 175 PKRLIVKLSGVPDRFTGSGGSDTFLKINRYAEADLGYVCMQGHSPLEFGAGTK 239
QY 240 LEIK 243
|||
Db 235 LEIK 238

RESULT 7
PCT-US00-19843-11
; Sequence 11, Application PC/TUS0019843
; GENERAL INFORMATION:
; APPLICANT: Herr, John C.

RESULT 10
US-09-364-088-16
; Sequence 16, Application US/09364088

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Db 87 APRFGKATFTDSSNTAYLQSLTSEDTAVAYCNEGTPGPY--FDYWGQGTIVT 143
 QY 114 VSSGGGGGGGGGGGGGSDVLMOTPTLLSVTIGOPASICKSSQSLDSDGKTYLNMILL 173
 Db 144 VSSGGGGGGGGGGGGGSENVLTQSPALMSASGEKVTITCSASSV-----SYNHWQ 197
 QY 174 QRPQSPKRLIYVSKLSDGVPPDFTGSGSGDTFTLKINVEADLGVIYVCMQGTSPLT 233
 Db 198 OKRGTSPKLMYISTSNLAVGVPARFSGSGSGTSTSLTISHMEADATAYCCOORSSYPLT 257
 QY 234 FGAGTKLEIK 243
 Db 258 FGAGTKLEIK 267

RESULT 2
 US-08-661-052-16
 ; Sequence 16, Application US/08661052
 ; Patent No. 5837243
 ; GENERAL INFORMATION:
 ; APPLICANT: Yashwant M. Deo
 ; APPLICANT: Joel Goldstein
 ; APPLICANT: Robert Graziano
 ; APPLICANT: Cheezian Somasundaram
 ; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, Suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109-1875
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/661,052
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/484,172
 ; FILING DATE: 07-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Arnold, Beth E.
 ; REGISTRATION NUMBER: 35,430
 ; REFERENCE/DOCKET NUMBER: MXI-043CP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)227-5941
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 553 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-661-052-16

Query Match 69.8%; Score 900; DB 2; Length 553;
 Best Local Similarity 68.7%; Pred. No. 4.8e-65;
 Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;

QY 2 VOLQSGALVNSGASVSKTASGPNIKDYHMYKORPQGLEWIGWIDPENGDTTEYA 61
 Db 278 IKLOQSGALVNSGTSVSKTASGPNIRKDYHMYKORPQGLEWIGWIDPENGDTTEYA 337
 QY 52 PRFGQATMTADSSNTAYLQSLTSEDTAVAYCNEGTPGPY--FDYDALDYWGQGTIVT 114
 Db 338 PRFGQATMTADSSNTAYLQSLTSEDTAVAYCNEGTPGPY--FDYWGQGTIVT 394

QY 115 SSGGGGGGGGGGGGGGSDVLMOTPTLLSVTIGOPASICKSSQSLDSDGKTYLNMILLQ 174
 Db 395 SSGGGGGGGGGGGGGGSENVLTQSPALMSASGEKVTITCSASSV-----SYNHWQ 448
 QY 175 RQPGSPKRLIYVSKLSDGVPPDFTGSGSGDTFTLKINVEADLGVIYVCMQGTSPLT 234
 Db 449 KRGTSPKLMYISTSNLAVGVPARFSGSGSGTSTSLTISHMEADATAYCCOORSSYPLT 508
 QY 235 GAGTKLEIK 243
 Db 509 GAGTKLEIK 517

RESULT 3
 US-09-184-658-63
 ; Sequence 63, Application US/09184658
 ; Patent No. 6030792
 ; GENERAL INFORMATION:
 ; APPLICANT: Otterness, Ivan G.
 ; APPLICANT: Mezes, Peter S.
 ; APPLICANT: Downs, James T.
 ; APPLICANT: Johnson, Kimberly S.
 ; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
 ; FILE REFERENCE: PC9946-A
 ; CURRENT FILING DATE: 1998-11-02
 ; EARLIER APPLICATION NUMBER: 60/065,423
 ; EARLIER FILING DATE: 1997-11-13
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 63
 ; LENGTH: 289
 ; TYPE: PRP
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
 ; OTHER INFORMATION: scfv.
 ; FEATURE:
 ; OTHER INFORMATION: Likely Initiator Met.
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (23)..(138)
 ; OTHER INFORMATION: 5109 VH domain.
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (139)..(154)
 ; OTHER INFORMATION: 16 amino acid linker.
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (155)..(266)
 ; OTHER INFORMATION: 5109 VL domain.
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (270)..(279)
 ; OTHER INFORMATION: myc tag.
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (284)..(289)
 ; OTHER INFORMATION: His tag.
 ; US-09-184-658-63

Query Match 65.4%; Score 843.5; DB 3; Length 289;
 Best Local Similarity 68.4%; Pred. No. 7.9e-61;
 Matches 167; Conservative 23; Mismatches 53; Indels 1; Gaps 1;

QY 1 OVQLOQSGALVNSGASVSKTASGPNIKDYHMYKORPQGLEWIGWIDPENGDTTEYA 60
 Db 23 EVQLVESGGGSGVQPGSKLSTCAASGFTFTNYGMSWVRQTPDKRLEWATINSNGLTFY 82

RESULT 4
US-08-331-398A-34
; Sequence 34, Application US/08331398A
; Patent No. 5608039

TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
 TITLE OF INVENTION: and Their Uses (as amended)
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Steuart Street Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/331,398A
 FILING DATE: 28-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 015280-1261100S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 OS-08-331-398A-34

Query Match	64.38;	Score 828.5;	DB 1;	Length 248;
Best Local Similarity	63.78;	Pred. No. 1.1e-59;		
Matches 156;	Conservative 34;	Mismatches 52;	Indels 3;	Gaps 1

RESULT 5
US-08-331-397B-34
; Sequence 34, Application US/08331397E

APPLICANT: Pastan, Ira
 TITLE OF INVENTION: Benhar, Itai
 TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
 TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Crew
 STREET: One Market Plaza, Steuart Street Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/331,397B
 FILING DATE: 128-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 015280-12612005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 248 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 OS-08-331-397B-34

Query Match	64.3%	Score 828.5;	DB 2;	Length 248;
Best Local Similarity	63.7%	Pred. No. 1.1e-59;		
Matches 156;	Conservative 34;	Mismatches 52;	Indels 3;	Gaps 1;

MOLECULE TYPE: protein
US-08-875-811-53

Query Match 63.0%; Score 812; DB 3; Length 365;
Best Local Similarity 61.7%; Pred. No. 3,5e-58;
Matches 150; Conservative 42; Mismatches 51; Indels 0; Gaps 0;

1 QVLOOQSGAEIVRSGASVYLSCTASGFNFKDYMHVWKORPEGLMIMIDPENGDTEY 60
119 QVRLQOQSGPELKRPGFTVSKASAGTFTNMGNNVKAQPGKGLKMGMINITYGESTY 178
61 APFQKATMTADTSNNTAVYLSLASEDTAVYYCNFYGDALDYMGQGTIVYSSGGG 120
179 ADFKRGAFASLETSAASAVYLSLASEDTAVYYCNFYGDALDYMGQGTIVYSSGGG 238
121 SGGGSGGGGSDVLMOTPLTSLVITIGQPASISCKSSQSLSDGKTYLNMILQRPQSP 180
239 SGGGSGGGGSDIVLTQSPFNPTLTGTSASISCRSTKSLHNSGITYLYWYLQKPGQSP 298
181 KRITIVSKLDSGVDPDRFTSGSGTDTLTKINRYEADLGYYCMQGTSHPLFFGAGTKL 240
299 QLLIYQMSNLASGVDPDRFSSSGSGTDTLTKISRYEADVGYYCAQNLPTPTFGGAGTKL 358
241 EIR 243
359 EIR 361

RESULT 8

US-08-875-811-55
Sequence 55, Application US/08875811
Patent No. 6045793

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02568
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-55

Query Match 63.0%; Score 812; DB 3; Length 365;
Best Local Similarity 61.7%; Pred. No. 3,6e-58;
Matches 150; Conservative 42; Mismatches 51; Indels 0; Gaps 0;

1 QVLOOQSGAEIVRSGASVYLSCTASGFNFKDYMHVWKORPEGLMIMIDPENGDTEY 60
2 QVRLQOQSGPELKRPGFTVSKASAGTFTNMGNNVKAQPGKGLKMGMINITYGESTY 61
61 APFQKATMTADTSNNTAVYLSLASEDTAVYYCNFYGDALDYMGQGTIVYSSGGG 120
62 ADFKRGAFASLETSAASAVYLSLASEDTAVYYCNFYGDALDYMGQGTIVYSSGGG 121
121 SGGGSGGGGSDVLMOTPLTSLVITIGQPASISCKSSQSLSDGKTYLNMILQRPQSP 180
122 SGGGSGGGGSDIVLTQSPFNPTLTGTSASISCRSTKSLHNSGITYLYWYLQKPGQSP 181
181 KRITIVSKLDSGVDPDRFTSGSGTDTLTKINRYEADLGYYCMQGTSHPLFFGAGTKL 240
182 QLLIYQMSNLASGVDPDRFSSSGSGTDTLTKISRYEADVGYYCAQNLPTPTFGGAGTKL 241
241 EIR 243
242 EIR 244

RESULT 9

US-08-279-772A-8
Sequence 8, Application US/08279772A
Patent No. 6080560

GENERAL INFORMATION:

APPLICANT: Russell, David R
APPLICANT: Fuller, James T
TITLE OF INVENTION: Method for Producing Antibodies in Plant
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
STREET: PO Box 2113
CITY: Madison
STATE: WI
COUNTRY: United States of America
ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,772A
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9097-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-279-772A-8

Query Match 62.4%; Score 804; DB 3; Length 239;

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 02:00:11 ; Search time 936.51 Seconds
(without alignments)
5589.469 Million cell updates/sec

Title: US-09-297-181-3

Perfect score: 747
Sequence: 1 caggtcaagctgcagagatc.....gcaccaagctggaatcaaa 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	261.2	35.0	1057	106	BE306420
2	221.4	29.6	641	90	AM4056821
3	214	28.6	533	95	AM802126
4	207	27.7	508	90	AM406572
5	206	27.6	630	90	AM406512
6	205.4	27.5	643	89	AM390292
7	204.4	27.4	358	136	BE850886
8	203.8	27.3	550	90	AM404610
9	202.2	27.1	644	106	BE281961
10	201.6	27.0	388	97	AM951579
11	201.6	27.0	507	139	BF015548
12	200.4	26.8	328	90	AM406484
13	199	26.6	464	107	BE368025
14	196.8	26.3	406	139	BF016722
15	193.6	25.9	459	89	AM383565
16	192.4	25.8	911	106	BE286958
17	190.4	25.5	379	96	AM908776
18	190.4	25.5	542	90	AM405977
19	190	25.4	349	97	AM947280
20	188.4	25.2	512	139	BF023434
21	186.2	24.9	460	90	AM406939
22	185.2	24.8	397	38	AV685287
23	185.2	24.8	401	38	AV685285
24	184.6	24.7	625	38	AV702633
25	184.2	24.7	739	106	BE284158
26	183.4	24.6	449	90	AM402364
27	182.6	24.4	443	139	BF015986
28	180.8	24.2	554	174	A2505978
29	180.6	24.2	363	5	AA300651
30	180.6	24.2	473	106	BE307170
31	179	24.0	323	90	AM407858
32	177.4	23.7	567	106	BE287568
33	177.4	23.7	596	106	BE310080
34	176.8	23.7	364	145	T27579
35	175.8	23.5	601	172	A2447391
36	175	23.4	549	139	BF022578
37	173.2	23.2	439	104	BE136816
38	172.2	23.1	594	106	BE309592
39	172	23.0	517	90	AM408270
40	171.8	23.0	488	90	AM403591
41	171.4	22.9	435	90	AM402541
42	169	22.5	448	90	AM402665
43	168.4	22.3	477	90	AM403686
44	166.4	22.3	398	87	AM4229526
45	165.4	22.1	457	90	AM405627

ALIGNMENTS

RESULT 1
 BE306420
 LOCUS BE306420 1057 bp mRNA
 DEFINITION 601103347F1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:3495755 5',
 mRNA sequence.
 ACCESSION BE306420
 VERSION BE306420.1 GI:9159604
 KEYWORDS EST.
 SOURCE house mouse.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1057)
NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM8546 row: n column: 12
High quality sequence stop: 695.
Location/Qualifiers

FEATURES

source

1. 1057
/organism="Mus musculus"
/strain="CZECH II (fetal)"
/db_xref="taxon:10090"
/clone="IMAGE:349575"
/clone_1ib="NCI CGAP Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT

274 a 289 c 273 g 221 t

ORIGIN

Query Match 35.0%; Score 261.2; DB 106; Length 1057;
Best Local Similarity 84.4%; Pred. No. 1.8e-66;
Matches 309; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

QY 2 aggtcaagctgcagagtcagggcagaaactgtgagtcaggggctcagtcattgt 61
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DB 78 AGGTCAGCTGCAGAGCTGCGGCGAGAGCTGTGAGCGGCGGCTCAGTCAAGTTG 137
QY 62 cctgcagagcttcgcttcacattaaagactacatagctgctggtgaacagagc 121
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DB 138 CCGCACAGCTTCGCTTCACATTAAAGACAGCCTTATGACACTGGGTGAACAGAGGC 197
QY 122 ctgaagaagggcctgagtgatgatatatctctgagagtggtgaaactgaatag 181
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DB 198 CTGAACAAGGCGCTGAGTGGATTGATGATTATCTGTGAGATGGTGAACATAATATG 257
QY 182 ccccgaaactccagggcagaaagccactgtgactgcagacacacactccaaacagcctacc 241
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DB 258 CCCGGAAGTCCAGGAAGGACCATATAGTCAGACACATCTCCAAACAGCGCTACC 317
QY 242 tgcacctcagagcctgacactgaggaacaaacgctctattactgtaatgacgtaactc 301
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DB 318 TGCAGCTCAGACCTGACACTCTGAGAGACACTCCACTCTTACTGCTGAGAAACCTTT 377
QY 302 actatgaatcagcagctatgcttgtagactggggcgaaggagacagagctacagctct 361
|||||
DB 367 TGTAT-----GGTGTACTAGCACTACTGGGCGCAAGGCACACACTATACAGCTCT 428
|||||

DEFINITION

UI-HF-BL0-abp-h-07-0-UI.r1 NIH-MGC_37 Homo sapiens CDNA clone
IMAGE:3057636 5', mRNA sequence.

ACCESSION

AM405821

VERSION

AM405821.1 GI:6924878

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 641)

AUTHORS

NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>

TITLE

Unpublished (1999)
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

COMMENT

Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbfp/image/image.html
Seq primer: M3 Forward..

FEATURES

source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3057636"
/clone_1ib="NIH-MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/note="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Beito Soares, Ph.D."

BASE COUNT

159 a 178 c 163 g 141 t

ORIGIN

Query Match 29.6%; Score 221.4; DB 90; Length 641;
Best Local Similarity 78.9%; Pred. No. 9.6e-55;
Matches 277; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 400 gttgctgagatcgacattagctacccagctctccatctccctggtgtgtgaagcaga 459
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DB 41 GGTGCTAGGCGGACATCTGATGACCCAGTCTCCAGACTCCCTGCTGTCTCGGCGC 100
QY 460 gagaagctgcctatgagctgcaaatccagtcagagtcgttcaacagtagaacccgaag 519
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DB 101 GAGAGGGCCACCATCAATGCAAGTCCACGCCAGAGCTTTATACAGCTCCAAACATAAG 160
QY 520 aattactgcttggtatagaagcaaacagagcgagctcccaagtgtgtactactg 579
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DB 161 AACTCTTATGTTGGATAGCAAGAAACAGGCGACCTCTTACGCTCATTTATCTGG 220
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DB 221 GCATCTACCCGGGAATCCGGGCTCTGACCATTCATGAGGCGGCGGCTGGGAAGAT 280
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DB 281 TTCACCTCAGCATCAGCAGCTGCAGCGTGAAGATGTGCGAGTTATATCTGACGAA 340
QY 700 tctta---taactaccagcgttcgagcgaggcgaacagctggaatcaaa 747
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DB 341 TATTATAGTACTCTCGAGCTTCGGCGCAGGGGACCAAGGTTGGAATCAAA 391
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Tue Feb
434

641 bp mRNA

EST

16-FEB-2000

RESULT	3
LOCUS	AM802126
DEFINITION	AM802126 533 bp mRNA EST 16-MAY-2000
ACCESSION	U5-UM0071-120400-055-d06 UM0071 Homo sapiens cDNA, mRNA sequence.
VERSION	AM802126
KEYWORDS	EST. GI:7853996
SOURCE	human.
ORGANISM	Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 533) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsushima,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.T. and Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE	2020263 Contact: Stimpson A.J.G. Laboratory of Cancer Genetics Rueg Institute for Cancer Research, Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@rueg.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.rueg.org.br/scripts/gethtml2.pl?cl=stc-U5-UM0071-120 400-065-d06&t3=2000-04-12&t4=1) Seq primer: puc 18 forward High quality sequence stop: 419.
FEATURES	Location/Qualifiers
SOURCE	1..533 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_idb="UM0071" /dev_stage="Adult" /note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
CASE COUNT	131 a 145 c 137 g 120 t
ORIGIN	

	Query Match	28.6%	Score 214:	DB 95:	Length 533:
	Best Local Similarity	77.7%	Pred. NO. 1.4e-52:		
	Matches 272:	Conservative 0:	Mismatches 75:	Indels 3:	Gaps 1:
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Dd	4 gtccgcagcggggcacatcmtgatgacctccagactccctgcctgctctggcgcg				
QY	461 agaaagtctcatatgctgcgcgaataatccagtcagagctgttcaacagtgtaaacccaaga				
Dd	64 AGAGGGCCACCTCACTGACAAGTCCAGCGCAGAAGTGTTATTATACGTCCACCAATAAAGA				
QY	521 attacttgtctgtgatcagcagaacaacaggcgcactctcctaagtctgtactactggy				
Dd	124 ACTACTTAGCTGTGATCACAGCAGAAACCAGGACAGCCTTCCTTAAGCTGCATTTACTGGG				
QY	561 catcaccaagggaatctcytagctcccttgatcgtcttacaggcagctgtgactctgggaagatt				
Dd	184 CATCTAACCCCGGAATCCGGGGCTCCCTGTGACCCGATTATAGTGGCAGCCGGGTCTGGGACAGATT				

[illegible]

RESULT	4
LOCUS	AM406572
DEFINITION	AM406572 508 bp mRNA EST 16-FEB-2000
ACCESSION	U1-HF-BL0-acu-g-10-0-0-UT.1 NH_MGC_37 Homo sapiens CDNA clone
VERSION	IMAGE:3060307 5, mRNA sequence.
KEYWORDS	AM406572
SOURCE	AM406572.1 GI:6925629
ORGANISM	EST.
	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 508)
AUTHORS	NH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
	Tel: (301) 496-1550
	Email: Robert.Strausberg@nih.gov
	Eco RI site shown at the beginning of the sequence.
	Tissue Procurement: Louis M. Straud, M.D., Ph.D.
	CDNA Library Preparation: M.B. Soares Lab
	CDNA Library Arrayed by: M.B. Soares Lab
	DNA Sequencing by: M.B. Soares Lab
	Clone distribution: MGC clone distribution information can be
	found through the I.M.A.G.E. Consortium/JLNL at:
	www-bio.lnl.gov/bdnp/image/image.html
	Seq primer: M13 forward.

FEATURES	SOURCE	location/Qualifiers
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		/cell_type="germinal center B cells"
		/cell_line="MGC85"
		/lab_host="DH10B (LRI)"
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BASE COUNT		115 a 139 c 126 g 128 t
ORIGIN		

	Query Match	Similarity	Score	DB	Length	
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	Matches	268; Conservative	0; Mismatches	80; Indels	3; Gaps	1;
QY	400	ggtgagatcagacattgagatcaccacagctccatctccctgctgtgtcagcagga	459			
Db	49	ggtgctcctacgggagacatcgatgtagaccacagctccctggctgtctctggggc	108			
QY	460	gagaaagtctgctatgagctgtcaaatccagctcaagatctgtttcaacagtagaacccggaag	519			
Db	109	gagagggccacatcatcaactgacgaagtcacagatggtttatpaaagctccaaacataag	168			
QY	520	aatactctggcttgctgtacacagaaacacagagcagctctccaaagtctgtactactgt	579			
Db	169	aaactccttaacttgtgtaccacactgaaacacagacagcctctcctaaatgatcatctttactgg	228			
QY	580	gcattccactagaggaatctgtaggtcccttgatcgcttcacagcagatgtgactctggaacagat	639			

Db	229	GCATCTACCCGGGAATCCGGGGTCCCTGACCATTTCAGTGCGAGCGGGTCTTGGACAGAT	288
Oy	640	ttaacttcaccatcaagcagtgtcgaggctgaagacgtgcgaatttatcttaccgaa	699
Db	289	TTCACTCCTCACCATGACGGCCCTGAGGCTGAAGATGTGGCAGTTATATCTGACGAA	348
Oy	700	tctatacttacg---acgttcggcggggccaccaagcttgaaatcaa	747
Db	349	TATCAATAGATATCCGTACACTTTTGGCCACGGGGACCAAGCTGTGAGATCAA	399
RESULT	5		
LOCUS	AM406512	630 bp	mRNA EST 16-FEB-2000
DEFINITION	UI-HF-BL0-acu-a-09-0-ui-rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060017 5', mRNA sequence.		
ACCESSION	AM406512		
VERSION	AM406512.1	GI:6925569	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLM at: www-bio.lnl.gov/bdrip/image/image.html Seq primer: M13 Forward.		
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	/clone_id="NIH_MGC_37"		
	/tissue_type="lymph"		
	/cell_type="germlinal center B cells"		
	/cell_line="MGC85"		
	/lab_host="DH10B (LT1)"		
	/note="Vector: pUT73-Pac; Site.1: NotI; Site.2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT	162 a 178 c 156 g 134 t		
ORIGIN			
Query Match	27.6%; Score 206; DB 90; Length 630;		
Best Local Similarity	75.4%; Pred. No. 3.5e-50;		
Matches	270; Conservative 0; Mismatches 85; Indels 3; Gaps 1;		
Oy	333	cctctgcggtgcygatcgacaattgagctcacccaagcttcacattccctcgtgtgtc	452
Db	1	CACGAGGGGTGCTTCACGGGGACATGTAATGCCAAGTCTCCAGACTCCCTGGCTGTGC	60
Oy	453	agcagaagaagagtcgcgtatgagctgcaaacccagtcgagctgtttcaacagtagaac	512
Db	61	TCTGGGCGAGAGGCCACCATCAATTCAGAAGTCCAGCCAGATCTTTTATACAGCTCCA	120
Oy	513	ccgaaaagaattacttgtgtgtatcagcagaaccaggcagctctcctaagtgctgat	572

Db	121	CAATAGAAATTCCTAGTTGGTACACAGAAACAGACAGCCTCCTTAAGCTGCTAT	180
Qy	573	ctactcgtccatccacataggaatctgtgagtcctcgtatcgtctcacaggcagtgtgac	632
Db	181	TTCTCGGGCAGTCATTACCCCGGAATCCGGGGTCCCTTACCCGATTCAGTGGCAGCGGCTGG	240
Qy	633	gacacattcactctccacatagcagctgtgaggtctaaagccctggcagttattactg	692
Db	241	GACAAATTTCAGCTCTCACACATCAGCAGCCTGAGGCTGAAGATGTGGCAGTTATTACTG	300
Qy	693	caagcaatctataatctacc---gacgtctggcggggcacaacagctggaatcaaa	747
Db	301	TCAGCAATATATATAGTATATTCCTTACCTTGGGCCAAGGACACAGACTGGAATTA	358
RESULT	6		
LOCUS	AM390292	643 bp	EST
DEFINITION	CM2-ST0182-221099-023-f04 ST0182 Homo sapiens cDNA, mRNA sequence.		04-FEB-2000
ACCESSION	AM390292		
VERSION	AM390292.1	GI:6894951	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 643)		
TITLE	HCGP http://www.ludwig.org.br/ORESTES .		
JOURNAL	The FAPESP/LICR Human Cancer Genome Project		
COMMENT	Unpublished (1999)		
	Contact: Simpson A.J.G.		
	Laboratory of Cancer Genetics		
	Ludwig Institute for Cancer Research		
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil		
	Tel: +55-11-2704922		
	Fax: +55-11-2707001		
	Email: asimpson@ludwig.org.br		
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?v1-CM2&t2-CM2-ST0182)		
	221099-023-f04&t3-1999-10-22&t4-1)		
	Seq primer: puc 18 forward		
	High quality sequence start: 7		
	High quality sequence stop: 641.		
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source	1..643		
	"/organism="Homo sapiens"		
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	"/clone_id="ST0182"		
	"/dev_stage="Adult"		
	"/note="Organ: stomach; Vector: puc18; Site:1: Smal; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application NO.196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	162 a 173 c 162 g 146 t		
ORIGIN			
Query Match	27.5%; Score 205.4; DB 89; Length 643;		
Best Local Similarity	76.1%; Pred. No. 5.3e-50;		
Matches	267; Conservative 0; Mismatches 81; Indels 3; Gaps 1;		
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Db	57	GGTGCTACGGGGACATCGTATGCCACAGCTCCAGACTCCCTGGCTGTCTGGGC	116
Qy	460	gagaagcgcgtatgagctcaaatcagctagagctgtgtcaaaagtagaacccgaag	519
Db	117	GAGAGGCCACATCACTGCAAGTGCAGCCAGAGATATTATTATCAACTCCAAATAAAG	176

Oy	520	aatctcttgagcttggtatcatcagcaagaacccagagcagctctccctaaagtgtcgtactcttg	579
Db	177	AACTACTTAAGCTTGGTATCCACGACGAAACCAAGACAGACCTCTCTTAAGCTGCTCTTTTACTGG	236
Oy	580	gcatccactaaggaatctggaatctccctgtatcgtcttcacagagcagctgagatctggtgacagat	639
Db	237	GCATCTACGCGGAAATCCGGGCTCCCTGACCGATTCAGTGCAGCGGCTGTGGACAGAT	296
Oy	640	ttcactcttaccatcagcagctgtgtcagcgttgaaagcttgccagttattacttcaagcaa	699
Db	297	TTCACTCTTCACATCAGCAGCGCTGCAGGGCTGAAGAAGTGTGGCAATTATTACTGTCCAG	356
Oy	700	tcctata--atctaccgagcttcggcggggagccacagctgaatctcaaa	747
Db	357	TATTTTAGTCATCTCTCAACGTTTCGGCCAAAGGACCAAGTGGAAATCAAA	407
RESULT	7		
LOCUS	BE850886		
DEFINITION	BE850886 358 bp mRNA	EST	26-SEP-2000
	uv89h05.v1 Soares mammary gland NMLNG Mus musculus cDNA clone		
	IMAGE:3469209.5' similar to SW:HV7_MOUSE P01751 IG HEAVY CHAIN V		
	REGION BI-8/186-2 PRECURSOR. ; mRNA sequence.		
ACCESSION	BE850886		
VERSION	BE850886.1	GI:10309225	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Euarchyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 358)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	This clone is available royalty-free through LNL ; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	GI:1388569		
	Seq primer: -40RP from Gibco.		
FEATURES	Location/Qualifiers		
source	1..358		
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	/clone_lib="Soares_mammary_gland_NMLNG"		
	/sex="female (lactating)"		
	/tissue_type="mammary gland"		
	/lab_host="DH10B"		
	/note="Vector: pRT73D-Pac (pharmacia) with a modified		
	polylinker. 1st strand cDNA was prepared from mammary		
	gland tissue from a lactating female, and was then primed		
	with a Not I - Oligo(dT) primer. Double-stranded cDNA was		
	ligated to Eco RI adaptors (Pharmacia), digested with Not		
	I and cloned into the Not I and Eco RI sites of the		
	modified pRT73 vector. Library is normalized. Library		
	was constructed by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	89 a 97 c 93 g 79 t		
ORIGIN			
Query Match	27.4%:	Score 204.4; DB 136; Length 358;	
Best Local Similarity	74.7%:	Pred. No. 8.8e-50;	
Matches	272; Conservative	0; Mismatches 86; Indels 6; Gaps 1	
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Db	1	CAGGTCCAACCTGCACACAGCCTGGGGCTGTGTAAGCCTGGGCTTCAGTGAAGCTG	60
Oy	61	tctctgacagcgtcttggtcctaaattaaagactactatgcatcaggtggaacagag	120

Query Match	Score	DB	Length
Best Local Similarity	75.8%	Pred. NO. 1.5e-49;	

Matches	266: Conservative	0: Mismatches	82: Indels	3: Gaps	1
Oy	400	gtgtgcgatgcgtgaacattgagctcaacccagcttccttcattccttcgtctgtgcagcaagaa	459		
Db	10	GGTGTCTACGGGGACATCTGTGATGACCAGTGTCCAGACTCCCTGGCTGTGTCTGGGC	69		
Oy	460	gagaagatgcgcattgagctgcgaatccagtcagagctcttcaacagtcagaaccgcgaag	519		
Db	70	GAGAGGCGCCACCATCAACTCGCAAGTCACCCAGCCAGAGTGTTTATACAGCTCCCAACATTAAG	129		
Oy	520	aattccttgcttgatatacagaagaaccagagcagtcctcctaagctgtgactctactctg	579		
Db	130	AACTACTTGTAGCTTGGATGACGACGAACACGAGACAGCCCTCTAAACTGCTCAATTTCGGG	189		
Oy	580	gcataccacaggaatctgtgagtcctcctgtgtgcttcacaagagagtgatcttgcgaagat	639		
Db	190	GGATTCATCCCGGGAAATCCGGGGTCCCTGTGACCAATTCAGTGCGAGCGGGTCTGGACAGAT	249		
Oy	640	ttcactctccaccatcagcagctgtgcagagctgaagacctgcagcttattacttcagaagca	699		
Db	250	TTTACCTCTCCACATCAGCAGCGCTGACGCTGGAAGATGTGGCAGTTTATATGTGTGCAAA	309		
Oy	700	tcttataatctacc---gaagcttcggcgagggacacaaagcttggaaatcaaa	747		
Db	310	TATTATAGTACTCCATCATCCTTCGGCCCAAGGAGACGATGAGATTTAA	360		
RESULT 9					
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DEFINITION	60109951891 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3492028	5'			
ACCESSION	BE281961				
VERSION	BE281961.1	GI:9157200			
KEYWORDS	EST				
SOURCE	house mouse.				
ORGANISM	Mus musculus.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 644)				
JOURNAL	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Tel: (301) 496-1550				
	Email: Robert.Strausberg@nih.gov				
	Tissue Procurement: Gilbert Smith, Ph.D.				
	cDNA Library Preparation: Life Technologies, Inc.				
	DNA Sequencing by: Incyte Genomics, Inc.				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
	Plate: LRAM8537 row: c column: 05				
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	/lab_host="DH10B"				
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	Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.				
	library constructed by Life Technologies. Investigator				
	providing samples: Gilbert Smith, NIH"				
BASE COUNT	147 a 176 c 155 g 166 t				
ORIGIN					

Query Match	27.1%	Score 202.2	DB 106	Length 644
Best Local Similarity	73.5%	Pred. No. 4,7e-49		
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Qy 1	caggtaacgctgcgaagagtcaggagggcagaacttgtaggtcaggagggcctcaagtcatttg 60			
Db 63	CAGGTTCACGTGCAACAGTCTGACCCTGAGTTGGACACCTGGAGCCTTCAGTGAAGATA 122			
Qy 61	tctgtacagcttcgtgtcctcaaccttaagactactatgatgccttggtggaacagag 120			
Db 123	TCTGTCAAGGTTCTGGCTACACCTTCACCTGACCACTACTATTCACCTGGGTAAGCAGAG 182			
Qy 121	ccctgaagagggcctgagtgatgtgatataattgatccctgagagtggttgaaactgaatc 180			
Db 183	CCGAAACAGGGCCTGGAATGAGATTGGATATATTATCTTAAGATGGTAGTACTAAGTAC 242			
Qy 181	ggcccgaaacttcaggggcagagccacgtgtgactgcagacacatccctccaaacagcctac 240			
Db 243	AATGAAAGATTCAAGGGCAGGCGCACATGTGACTGCAAGATTAATCTCCAGACATGCCTTC 302			
Qy 241	ctgcacctgaagggcctgacatctatgaagacacacccgctactactgt-----aatgca 294			
Db 303	ATGCAGCTCACAGCCTGCATCTTAGAGTTTCTGCAGTGTATTCTGTGCAAGAGGGGGA 362			
Qy 295	gtcatctactatgaatcacagcgctatgctttggaacttggggcgaaggaccagagtc 354			
Db 363	TTCATCTACATGATGTTACGGCCTCTACTACTGTTGACTACTGGCGCCAAAGGACCACTATC 422			
Qy 355	accgctctccctcag 367			
Db 423	ACAGTCTCCTCAG 435			
RESULT 10				
LOCUS	AM951579	388 bp	mrna	EST 01-JUN-2000
DEFINITION	EST363649 MAGE resequences, MAGB Homo sapiens cDNA, mRNA sequence.			
ACCESSION	AM951579			
VERSION	AM951579.1	GI:8141256		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 388)			
AUTHORS	H.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J			
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301.838.3528 Fax: 301.838.0208 Email: jshnq@tigr.org Plate: 29			
FEATURES	Seq primer: Reverse.			
source	1. 388			
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	"/note="Vector: pBluescriptKm"			
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Best Local Similarity	75.6%	Pred. No. 5.3e-49		

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Db	40	GGTGCTAGGGGGAGACCGGTATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTTG6GC	99
QY	460	gagaagtgctgctatgaagctgcaaatccagtaagctctgttcaacaagtaagaaccgaag	519
Db	100	GAGAGGGCCACATCAATGACGTGACGGTCCAGCCAGAGTGTTTAGACAGCTCCAAACATACG	159
QY	520	aattactgtgcttgtatcaagcagaaccaaaggagcttcctaaagtgtgattctacttg	579
Db	160	AACCTACTAGCTGTGTACCAACTGAACACGAGACAGCCTCTAAGCTGTGCTATTTACTGG	219
QY	580	gcattccactaaggaaatcctggaagtcctctgattcctcaagcagtgatctggaagat	639
Db	220	GCATCTACCCGGGAATCCGGGGGTCCCTGACGATTCATGTGACACGGGGTCTGGGACAGAT	279
QY	640	ttcaacttcacacatcagcagagtgtgcaggcttaagaacctggaattttactgaacaa	699
Db	280	TTCACTCTACCCCTCAGGGGCTCGAGGCTGAAGAATGGAGATTATTTACTGTCAACAA	339
QY	700	tcttaatactcacg---agcttgagcggggacccaagctggaataca	745
Db	340	TATTATTACTCCGTACAATTTTGGCCAGGGGACCAAGCTGGGAATCA	388

DEFINITION	LOCUS	507 bp	mRNA	EST	10-OCT-2000	IMAGE:3658670
BF015548	BF015548					
RESULT 11						

ACCESSION	BF015548	GI:10746880
VERSION	BF015548.1	
KEYWORDS	EST.	

SOURCE ORGANISM

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 507)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMU at: image.llnl.gov/image/html/resources.shtml

MGT:1421142
Seq primer: -40RP from G1bco
High quality sequence stop: 456.

FEATURES

source

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/strain="C2ECH II"
/db_xref="taxon:10090"
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Query Match	27.0%;	Score 201.6;	DB 139;	Length 507;
Best Local Similarity	73.6%;	Pred. No. 6.6e-49;		
Matches 271;	Conservative 0;	Mismatches 94;	Indels 3;	Gaps 1

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Db	93	AGGTCAACCTC	CACACAGCT	CTGAGCT	GAGTGGGAAG	CGCTGGGGCTT	CAGTGAAGATAT	150				
QY	62	cctgcacagact	ctctgtgc	ttcaacata	aagactacta	taigtac	tgggtg	gaaacaga	ggc	121		
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QY	122	ctgaaagggg	ccctggagt	gtgattg	atgataat	tgtacctgt	gagtgagtg	ggtggaac	cgaatg	181		
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Db	333	TGGAGCTCA	AAGCGCTG	CATCTG	AGCATCTG	AGGACGTCTG	CATTTACTGT	GCAAGATAT	392			
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QY	362	ccctcaggt	369									
Db	450	CCTCAGCT	457									

RESULT	12
AM406484	
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DEFINITION	UI-HF-BL0-scr-f-09-0-ui.r1 NIH_MGC_37 Homo sapiens cDNA clone
ACCESSION	IMAGE:306032 5' mRNA sequence.
VERSION	AM406484.1 GI:6925541

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 328)				
NIH-MGC		http://www.ncbi.nlm.nih.gov/MGC/		
Unpublished (1999)		National Institutes of Health, Mammalian gene Collection (MGC)		
Contact: Robert Strausberg, Ph.D.				

FEATURES
source 1.328

Email: Robert.Strausser@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINt at:
www.bio.llnl.gov/dbp/IMAGE/IMAGE.html
Seq primer: M13 forward.
Location/Qualifiers

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/cell_line="MGC85"
/lab_host="DH10B (LT1)"

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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:24:31 ; Search time 42.85 seconds
(without alignments)
681.092 Million cell updates/sec

Title: US-09-297-181-4
Perfect score: 1315
Sequence: 1 QVKLOESGAEIVRSAGSVNL.....YCKOSYNLPTFGGKTLEIK 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP TREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_phage:*
10: sp_plant:*
11: sp_rentent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	744.5	56.6	298	11 Q9YF0	Q9YF0 mus musculu
2	433.5	33.0	109	11 Q9JL85	Q9JL85 mus musculu
3	384	29.2	118	11 Q9ZIC4	Q9ZIC4 mus musculu
4	379.5	28.3	117	11 Q9QX69	Q9QX69 mus musculu
5	374	28.4	107	4 Q9JL81	Q9JL81 homo sapien
6	370	28.4	124	4 Q9JL92	Q9JL92 homo sapien
7	370	28.1	109	4 Q9JL78	Q9JL78 homo sapien
8	368.5	28.0	99	11 Q9JL74	Q9JL74 mus musculu
9	368.5	28.0	108	4 Q9JL70	Q9JL70 homo sapien
10	368	28.0	110	11 Q9JL77	Q9JL77 mus musculu
11	367.5	27.9	117	11 Q9QX60	Q9QX60 mus musculu
12	367	27.9	114	11 Q9JL81	Q9JL81 mus musculu
13	365.5	27.8	108	4 Q9JL77	Q9JL77 homo sapien
14	363.5	27.6	108	4 Q9JL79	Q9JL79 homo sapien
15	359	27.3	109	11 Q9JL75	Q9JL75 mus musculu
16	355	27.0	109	4 Q9JL85	Q9JL85 homo sapien
17	351.5	26.7	108	4 Q9JL83	Q9JL83 homo sapien
18	349.5	26.6	119	4 Q9JL94	Q9JL94 homo sapien
19	348.5	26.5	125	4 Q9JL95	Q9JL95 homo sapien

20	347.5	26.4	150	4 Q9Y298	Q9Y298 homo sapien
21	342	26.0	104	11 Q9JL82	Q9JL82 mus musculu
22	338	25.7	109	4 Q9JL86	Q9JL86 homo sapien
23	334.5	25.4	117	11 Q9ZIC6	Q9ZIC6 mus musculu
24	334.5	25.4	214	11 Q9JL85	Q9JL85 mus musculu
25	331.5	25.2	114	4 Q9JL80	Q9JL80 homo sapien
26	313.5	23.8	101	11 Q9JL78	Q9JL78 mus musculu
27	311.5	23.7	103	11 Q9JL80	Q9JL80 mus musculu
28	309.5	23.5	107	11 Q9JL84	Q9JL84 mus musculu
29	309	23.5	116	4 Q9JL89	Q9JL89 homo sapien
30	306	23.3	110	11 Q9JL83	Q9JL83 mus musculu
31	306	23.3	147	4 Q9Y509	Q9Y509 homo sapien
32	305.5	23.2	113	4 Q9JL90	Q9JL90 homo sapien
33	305	23.2	106	5 Q9JL10	Q9JL10 schistosoma
34	302.5	23.0	131	4 Q9JL88	Q9JL88 homo sapien
35	301.5	22.9	116	4 Q9JL79	Q9JL79 homo sapien
36	300.5	22.9	119	4 Q9JL73	Q9JL73 homo sapien
37	300.5	22.9	121	4 Q9JL71	Q9JL71 homo sapien
38	296.5	22.5	97	11 Q9JL76	Q9JL76 mus musculu
39	296.5	22.5	157	4 Q95978	Q95978 homo sapien
40	288.5	21.9	109	6 Q9JL05	Q9JL05 oryctolagus
41	286	21.7	150	4 Q95973	Q95973 homo sapien
42	285	21.7	118	4 Q9JL91	Q9JL91 homo sapien
43	285	21.6	118	4 Q9JL72	Q9JL72 homo sapien
44	284	21.6	124	6 Q9JL06	Q9JL06 oryctolagus
45	282	21.4	124	6 Q9JL04	Q9JL04 oryctolagus

ALIGNMENTS

RESULT 1
ID Q9YF0 PRELIMINARY: PRT: 298 AA.
Q9YF0

AC Q9YF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DI 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CN 8 SCFV.

GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RT antibody recognizing a cell polarity using a phase display subtraction
RT method.";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB036341; BAA8633.1; -;
DR HSSP: P01607; IRLI.
DR INTERPRO: IPR003006; -;
DR PFM: PFM0047; Ig: 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 56.6%; Score 744.5; DB 11; Length 298;
Best Local Similarity 56.4%; Pred. No. 7.4e-58;
Matches 141; Conservative 37; Mismatches 61; Indels 11; Gaps 3;

QY 1 QVKLOESGAEIVRSAGSVNLCTASGFNKKDYMHVKKRPEGLWIGTIPSESTY 60
DB 40 QVKLOESGAEIVRSAGSVNLCTASGFNKKDYMHVKKRPEGLWIGTIPSESTY 99
QY 61 APNFGKATVFDTSSTAYLHLISLTSSTDTYYCNNAVYYEYDGYALDYGQGTTVTV 120

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035033; AAD56269.1; -.
 DR HSSP; P80362; 1MTL.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; 19; 1.
 DR NON_TER 1 1
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 28.4%; Score 374; DB 4; Length 107;
 Best Local Similarity 61.6%; Pred. No. 8.2e-26;
 Matches 69; Conservative 22; Mismatches 15; Indels 6; Gaps 1;

OY 138 DIELTOSPSLAVSAGEKVMKSSOSLFSNSTRKNYLAWYQKQKQSPKLYWASTR 197
 DB 1 DIGNOTSPSLASVSGRVTITCRASQSI-----SNYLWYQKQKQKAPNLITVYASSL 54
 OY 198 ESGVPRFSGSGGDTFTLTISVQAEDLAVYCKOSYNLPTFGGKLEIK 249
 DB 55 QSGVPRFSGSGGDTFTLTISGLQAEDEFTYCCOQSYSLTFEGTKVDIR 106

RESULT 6
 O9UL92 PRELIMINARY; PRT; 124 AA.
 AC O9UL92;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE 01-JUN-2000 (TREMBLrel. 14, last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035022; AAD56238.1; -.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; 19; 1.
 DR NON_TER 1 1
 FT NON_TER 124 124
 SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 28.4%; Score 373; DB 4; Length 124;
 Best Local Similarity 56.5%; Pred. No. 1.2e-25;
 Matches 70; Conservative 16; Mismatches 36; Indels 2; Gaps 1;
 OY 1 QVQLSSGALVSAAGSYNLSCTASGFNIDYMMHWKQPEEGLEGWIGITPESEGETEY 60
 DB 1 EYLVESGAEVKKPKGASVSKASGYTSSYYMHVROAPGGGLEMMGIIINSGGSTY 60

OY 61 ADFQKATVADTSSNTAYLHLSLTSEDYVYCNAYIYEYD--YALDYGQGTIV 118
 DB 61 ADFQKATVADTSSNTAYLHLSLTSEDYVYCNAYIYEYD--YALDYGQGTIV 120
 OY 119 TVSS 122
 DB 121 TVSS 124

RESULT 7
 O9UL78 PRELIMINARY; PRT; 109 AA.
 AC O9UL78;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035036; AAD56272.1; -.
 DR HSSP; P01789; 1MCP.
 DR INTERPRO; IPR003006; -.
 DR PFAM; PF00047; 19; 1.
 DR NON_TER 1 1
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 28.1%; Score 370; DB 4; Length 109;
 Best Local Similarity 62.8%; Pred. No. 1.9e-25;
 Matches 71; Conservative 22; Mismatches 14; Indels 6; Gaps 2;
 OY 138 DIELTOSPSLAVSAGEKVMKSSOSLFSNSTRKNYLAWYQKQKQSPKLYWASTR 197
 DB 1 EYLVESGAEVKKPKGASVSKASGYTSSYYMHVROAPGGGLEMMGIIINSGGSTY 60
 OY 198 ESGVPRFSGSGGDTFTLTISVQAEDLAVYCKOSYNLPTFGGKLEIK 249
 DB 56 ADFQKATVADTSSNTAYLHLSLTSEDYVYCNAYIYEYD--YALDYGQGTIV 108

RESULT 8
 O9UL74 PRELIMINARY; PRT; 99 AA.
 AC O9UL74;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Balb/C;
 RA Maltiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF206032; AAF69330.1; -.
 DR NON_TER 1 1
 FT NON_TER 99 99

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF206025; AAF69323.1; -
 FT NON_TER 1 114
 FT 1 114
 SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match 27.9%; Score 367; DB 11; Length 114;
 Best Local Similarity 61.1%; Pred. No. 3.7e-25;
 Matches 69; Conservative 12; Mismatches 32; Indels 0; Gaps 0;

OY 10 ELVRSASVNLSTAGFENIKDYMHVWVQRPESGLEWIGYIDPESGEFEYAPNFGKAT 69
 DB 2 QLVKPGASVVKISKAGYSTSTYMHVWVQRPESGLEWIGIDPSETRLNOKFKDKAT 61
 OY 70 VYADSSNTAYLHLSSLTSEDITVYCNVYIYEDYDALDYGGCTTVVSS 122
 DB 62 LTVKSSSTAYVQLSSPTSEDSAVYCCARSNYGSSLYYEDYVGGCTTLTVSS 114

RESULT 13
 ID 09UL77 PRELIMINARY; PRT; 108 AA.
 AC 09UL77;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035037; AAD56273.1; -
 DR HSSP; P01607; 1RET.
 DR INTERPRO: IPR003006; -
 DR PFAM; PF00047; 19; 1.
 FT NON_TER 1 108
 FT 1 108
 SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 27.8%; Score 365.5; DB 4; Length 108;
 Best Local Similarity 61.9%; Pred. No. 4.6e-25;
 Matches 70; Conservative 21; Mismatches 15; Indels 7; Gaps 2;

OY 138 DIELTSPSSLAWSAGEKAMKSSOSLFNSRTRKNYLAWYQKPGOSPKYLIYASR 197
 DB 1 DIOMTSPSSLSASVGDRTYITCRASOSI-----SYLAWYQKPGKAPNLLIYASL 54
 OY 198 EGGVPRFTGSGSGDTFTLTSSVQAEDLAVYCKOSYNL-PTFGGKYLEIK 249
 DB 55 QSGVPRFSGSGGDTFTLTSSLOPEDFATYCCQGSYSWTFGSGTKEIK 107

RESULT 14
 ID 09UL79

ID 09UL79 PRELIMINARY; PRT; 108 AA.
 AC 09UL79;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035035; AAD56271.1; -
 DR HSSP; P01607; 1RET.
 DR INTERPRO: IPR003006; -
 DR PFAM; PF00047; 19; 1.
 FT NON_TER 1 108
 FT 1 108
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 27.6%; Score 363.5; DB 4; Length 108;
 Best Local Similarity 61.9%; Pred. No. 7e-25;
 Matches 70; Conservative 19; Mismatches 17; Indels 7; Gaps 2;

OY 138 DIELTSPSSLAWSAGEKAMKSSOSLFNSRTRKNYLAWYQKPGOSPKYLIYASR 197
 DB 1 DIOMTSPSSLSASVGDRTYITCRASOSI-----SYLAWYQKPGKAPNLLIYASL 54
 OY 198 EGGVPRFTGSGSGDTFTLTSSVQAEDLAVYCKOSYNL-PTFGGKYLEIK 249
 DB 55 QSGVPRFSGSGGDTFTLTSSLOPEDFATYCCQGSYSWTFGSGTKEIK 107

RESULT 15
 ID 09UL75 PRELIMINARY; PRT; 109 AA.
 AC 09UL75;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF206031; AAF69329.1; -
 FT NON_TER 1 109
 FT 1 109
 SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 27.3%; Score 359; DB 11; Length 109;
 Best Local Similarity 59.8%; Pred. No. 1.8e-24;
 Matches 70; Conservative 16; Mismatches 19; Indels 12; Gaps 3;

OY 10 ELVRSASVNLSTAGFENIKDYMHVWVQRPESGLEWIGYIDPESGEFEYAPNFGKAT 69
 DB 1 ELVKGASVVKISKAGYSTSTYMHVWVQRPESGLEWIGYINPYNDGTKEKFKGKAT 60

Tue Feb 20 06:37:16 2001

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Page 6

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Qy      70 VTADTSNTAYLHLSLTSEPTVYVC-----NAVITYEYDGLADYWGQGTIVTSS 122
        :|:| |:||: |||||: ||| | | | |||||:||||
Db      61 LTSDKSSSTAYMELSLTSEDSAVYYCARDGN-----YRGF--DYWGQGTTLTVSS 109
```

Search completed: February 12, 2001, 15:24:31
Job time: 101 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:25:01 ; Search time 26.51 seconds

(without alignments)
637.769 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315

Sequence: 1 QVKLQESGALVRSASVNL.....YKOSYNLPFGGKLEIK 249

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857	65.2	268	A56446	Ig heavy chain V r
2	854.5	65.0	249	S41374	single chain Fv an
3	841.5	64.0	233	JC3322	p53 specific singl
4	544	41.4	112	S43103	Ig kappa chain V-J
5	538	40.9	113	PT0407	Ig light chain V r
6	533	40.5	112	PL0265	Ig kappa chain V r
7	533	40.5	133	PS0023	Ig kappa chain pre
8	520	39.5	113	PT0408	Ig light chain V r
9	514	39.1	112	S41393	Ig heavy chain V r
10	503.5	38.3	111	S03304	Ig kappa chain V r
11	501.5	38.1	106	S04576	Ig heavy chain pre
12	498	37.9	134	PH1101	Ig light chain V r
13	497	37.8	103	PH1047	Ig light chain V r
14	497	37.8	104	PH1102	Ig light chain V r
15	492	37.4	103	PH1051	Ig light chain V r
16	492	37.4	103	PH1052	Ig light chain V r
17	492	37.4	104	PH1104	Ig light chain V r
18	491	37.3	103	PH1050	Ig light chain V r
19	489.5	37.2	220	A31790	Ig kappa chain V r
20	489	37.2	120	G33932	Ig kappa chain pre
21	486	37.0	135	S38807	Ig light chain V r
22	486	37.0	178	S29594	Ig gamma chain (WM
23	484.5	36.8	113	PI0263	Ig kappa chain V r
24	484	36.8	101	PH1046	Ig light chain V r
25	484	36.8	104	PH1103	Ig light chain V r
26	480	36.5	111	G30502	Ig kappa chain V r
27	479	36.4	118	PT0356	Ig kappa chain V r
28	478.5	36.4	134	PC1214	Ig kappa chain pre
29	477.5	36.3	117	S17586	Ig heavy chain V r

30	477.5	36.3	214	2	S68212	Ig kappa chain (Ma
31	475	36.1	138	2	S26040	Ig kappa chain pre
32	474.5	36.1	113	2	PL0264	Ig kappa chain V r
33	474.5	36.1	120	2	S03471	Ig heavy chain V-D
34	470.5	35.9	240	2	S06084	Ig kappa chain pre
35	469	35.7	122	2	S06823	Ig heavy chain V r
36	468.5	35.6	112	2	E30538	Ig kappa chain V r
37	468.5	35.5	112	2	E30538	Ig kappa chain V r
38	468	35.6	116	2	S15672	Ig heavy chain V r
39	467.5	35.6	113	2	JC2270	PL7-6 antibody lig
40	467.5	35.6	118	2	S25174	Ig heavy chain V r
41	467	35.5	221	2	S49220	Ig gamma-1 chain -
42	466	35.4	112	2	S09970	Ig kappa chain V-J
43	465	35.4	97	2	A42575	Ig kappa chain V r
44	464	35.3	133	1	K4HUJ1	Ig kappa chain pre
45	463.5	35.2	113	2	S30520	Ig kappa chain V r

ALIGNMENTS

RESULT 1
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Rang, P.M.; Poltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270: 7829-7835, 1995
U.Title: A high affinity diopxin-binding protein displayed on M13 is functionally ide
A:Reference number: A56446; MUID:95229583
A:Accession: A56446
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:Cross-references: CB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match 65.2%; Score 857; DB 2; Length 268;

Best Local Similarity 66.8%; Pred. No. 3.1e-54;

Matches 167; Conservative 26; Mismatches 45; Indels 12; Gaps 3;

QY 1 QVKLQESGALVRSASVNLCTAGFNKDYMMHVKORPEGLWITGIDPESGETEY 60
DB 3 QVKLQESGALVRSASVNLCTAGFNKDYMMHVKORPEGLWITGIDPESGETEY 62
QY 61 APNFGKATVTDTSNTAYLHLSLTSEDTVYVCNAVYYEYDGYALDWGQGTVTYV 120
DB 63 DKPFGKATVTDTSNTAYLHLSLTSEDTVYVCNAVYYEYDGYALDWGQGTVTYV 118
QY 121 SSGGGSGGGGSGGGGSDIELTQSSSLAVSAGEVYVNSCKSSQSLFNSRTKNTLAWQ 180
DB 119 SSGGGSGGGGSGGGGSDIELTQSSSLAVSAGEVYVNSCKSSQSLFNSRTKNTLAWQ 171
QY 181 OKPGSPKVLITWASTRESGVDPRTSGSGGTFDLITLITSSVVAEDLAVYVCKOSNLP-T 239
DB 172 OKSDSPKVLITWASTRESGVDPRTSGSGGTFDLITLITSSVVAEDLAVYVCKOSNLP-T 231
QY 240 FGGGKLEIK 249
DB 232 FGGGKLEIK 241

RESULT 2

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Aitsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti

J. Exp. Med. 171, 265-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: P10231; MUID:90111618
 A:Accession: P10265
 A:Molecule type: mRNA
 A:Residues: 1-112 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-23/Region: framework 1
 F:16-96/Domain: immunoglobulin homology <IMM>
 F:24-40/Region: complementarity-determining 1
 F:41-55/Region: framework 2
 F:56-62/Region: complementarity-determining 2
 F:63-94/Region: framework 3
 F:95-102/Region: complementarity-determining 3
 F:103-112/Region: framework 4

Query Match 40.5%; Score 533; DB 2; Length 112;
 Best Local Similarity 92.0%; Pred. No. 1.4e-31;
 Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 138 DIELTSPSSSLAVSAGEKYAMCKSSQSLFNSTRKNTLAWYQKPGSPKLIYASTR 197
 ||:|||||
 Db 1 DIYMSQSPSSSLAVSAGEKYAMCKSSQSLFNSTRKNTLAWYQKPGSPKLIYASTR 60

QY 198 ESGVPRFTGSGSGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGKTLEIK 249
 ||:|||||
 Db 61 ESGVPRFTGSGSGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGKTLEIK 112

RESULT 7
 Ig kappa chain precursor V region (6A4) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
 C:Accession: PS00023
 R:Margaret, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
 Gene 74, 335-345, 1988
 A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
 A:Reference number: PS00023; MUID:89232725
 A:Accession: PS00023
 A:Molecule type: mRNA
 A:Residues: 1-133 <MAR>
 A:Experimental source: strain BALB/c
 A:Note: the amino-terminal four residues of the mature protein were directly sequenced
 C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aeruginosa
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-133/Product: ig kappa chain V region 6A4 #status experimental <IGV>
 F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 40.5%; Score 533; DB 2; Length 133;
 Best Local Similarity 89.7%; Pred. No. 1.7e-31;
 Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 134 GGGSDIELTSPSSSLAVSAGEKYAMCKSSQSLFNSTRKNTLAWYQKPGSPKLIYASTR 193
 ||:|||||
 Db 17 GCGCDIYMSQSPSSSLAVSAGEKYAMCKSSQSLFNSTRKNTLAWYQKPGSPKLIYASTR 76

QY 194 ASTRESGVPRFTGSGSGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGKTLEIK 249
 ||:|||||
 Db 77 ASTRESGVPRFTGSGSGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGKTLEIK 132

RESULT 8
 Ig light chain V region (S107/VH11 group 1-6) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PT0408

R. Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharif, M.D.
 J. Exp. Med. 173, 731-741, 1991
 A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantib
 A:Reference number: P10376; MUID:91147903
 A:Accession: PT0408
 A:Molecule type: DNA
 A:Residues: 1-113 <BEN>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 520; DB 2; Length 113;
 Best Local Similarity 90.2%; Pred. No. 1.2e-30;
 Matches 101; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 138 DIELTSPSSSLAVSAGEKYAMCKSSQSLFNSTRKNTLAWYQKPGSPKLIYASTR 197
 ||:|||||
 Db 1 DIYMSQSPSSSLAVSAGEKYAMCKSSQSLFNSTRKNTLAWYQKPGSPKLIYASTR 60

QY 198 ESGVPRFTGSGSGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGKTLEIK 249
 ||:|||||
 Db 61 ECGVPRFTGSGSGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGKTLEIK 112

RESULT 9
 Ig kappa chain V region (12.5H VL) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S41393
 R:Margaret, C.; Gilbert, D.; Brard, F.; Tron, F.
 submitted to the EMBL Data Library, January 1994
 A:Description: Structural characterization of an (NZB x NZW)F1 mouse-derived IgM anti
 A:Reference number: S41393
 A:Accession: S41393
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-112 <MAR>
 A:Cross-references: EMBL:Z29536
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 514; DB 2; Length 112;
 Best Local Similarity 88.4%; Pred. No. 3.1e-30;
 Matches 99; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 138 DIELTSPSSSLAVSAGEKYAMCKSSQSLFNSTRKNTLAWYQKPGSPKLIYASTR 197
 ||:|||||
 Db 1 DIYMSQSPSSSLAVSAGEKYAMCKSSQSLFNSTRKNTLAWYQKPGSPKLIYASTR 60

QY 198 ESGVPRFTGSGSGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGKTLEIK 249
 ||:|||||
 Db 61 DSGVPRFTGSGSGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGKTLEIK 112

RESULT 10
 Ig kappa chain V region (61B8) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
 C:Accession: S03304; JI0043
 R:Van Cleave, V.H.; Naeye, C.W.; Metzger, D.W.
 J. Exp. Med. 167, 1841-1848, 1988
 A:Title: Do antibodies recognize amino acid side chains of protein antigens indepen
 A:Reference number: JI0043; MUID:88258372
 A:Accession: S03304
 A:Molecule type: mRNA
 A:Residues: 1-111 <VAN>
 A:Cross-references: EMBL:X12380; NID:952341; PIDN:CAA30938.1; PID:9930189
 A:Note: the authors translated the codon GAT for residue 76 as Asn

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2001, 15:26:39 ; Search time 16.14 Seconds
(without alignments)
498.217 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315
Sequence: 1 QVRLQESGAEIVRSASVNL.....YCKQSYNLPTFGGTRLEIK 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	464	35.3	133	KVAB_HUMAN	P06133 homo sapien
2	463.5	35.2	134	KVAC_HUMAN	P06314 homo sapien
3	448.5	34.1	114	KVAA_HUMAN	P01625 homo sapien
4	418	31.8	121	KV40_HUMAN	P06312 homo sapien
5	400	30.4	139	HV07_MOUSE	P01751 mus musculu
6	393.5	29.9	114	KVIA_MOUSE	P01632 mus musculu
7	393.5	28.9	120	HV03_MOUSE	P01747 mus musculu
8	380.5	28.9	149	KV5A_MOUSE	P01633 mus musculu
9	378.5	28.8	136	KV5B_MOUSE	P01634 mus musculu
10	378	28.7	137	HV11_MOUSE	P01755 mus musculu
11	376.5	28.6	140	HV02_MOUSE	P01746 mus musculu
12	373.5	28.6	121	HV01_MOUSE	P01745 mus musculu
13	371.5	28.3	129	KV1M_HUMAN	P04431 homo sapien
14	369.5	28.1	108	KV1M_HUMAN	P01600 homo sapien
15	367.5	27.9	108	KV1C_HUMAN	P01744 homo sapien
16	366	27.8	143	HV1C_HUMAN	P80362 homo sapien
17	365.5	27.8	108	KV1Y_HUMAN	P01664 mus musculu
18	365.5	27.8	111	KV3L_MOUSE	P01756 mus musculu
19	365.5	27.8	117	HV12_MOUSE	P01757 mus musculu
20	363	27.6	109	KV3F_HUMAN	P18135 homo sapien
21	362	27.5	129	KV3L_HUMAN	P18135 homo sapien
22	361.5	27.5	108	KV1V_HUMAN	P04430 homo sapien
23	361.5	27.5	111	KV3R_MOUSE	P01670 mus musculu
24	361	27.5	109	KV3B_HUMAN	P01620 homo sapien
25	361	27.5	103	KV3D_HUMAN	P01622 homo sapien
26	361	27.5	113	KV2G_MOUSE	P06309 mus musculu
27	360	27.4	117	HV13_MOUSE	P01757 mus musculu
28	359.5	27.3	117	HV13_MOUSE	P06329 mus musculu
29	359	27.3	120	HV50_MOUSE	P01673 mus musculu
30	358.5	27.3	111	KV30_MOUSE	P04207 homo sapien
31	357	27.1	129	KV3M_HUMAN	P18136 homo sapien
32	357	27.1	129	KV3M_HUMAN	P01614 homo sapien
33	356.5	27.1	115	KV2A_HUMAN	P01614 homo sapien

34	355	27.0	108	1	KV3A_HUMAN	P01619 homo sapien
35	354.5	27.0	111	1	KV3T_MOUSE	P01672 mus musculu
36	354.5	27.0	138	1	HV3T_MOUSE	P03980 mus musculu
37	354	26.9	107	1	KV1D_HUMAN	P01596 homo sapien
38	354	26.9	110	1	KV3P_MOUSE	P01668 mus musculu
39	353.5	26.9	111	1	KV3S_MOUSE	P01671 mus musculu
40	353	26.8	118	1	HV51_MOUSE	P06330 mus musculu
41	352.5	26.8	108	1	KV1P_HUMAN	P01608 homo sapien
42	352.5	26.8	108	1	KV3Q_MOUSE	P01649 mus musculu
43	352.5	26.8	111	1	KV3O_MOUSE	P01667 mus musculu
44	352	26.8	109	1	KV3E_HUMAN	P01623 homo sapien
45	352	26.8	113	1	KV2D_HUMAN	P01617 homo sapien

ALIGNMENTS

RESULT	ID	QUERY	STANDARD	PRT	AA
1	KV4B_HUMAN				
AC	P06313:				
DT	01-JAN-1988 (Rel: 06, Created)				
DT	01-JAN-1988 (Rel: 06, Last sequence update)				
DT	15-JUL-1999 (Rel: 38, Last annotation update)				
DE	IG KAPPA CHAIN V-IV REGION JI PRECURSOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86041853; PubMed=2997712;				
RA	Klobeck H.G., Bojnacki G.W., Combrato G., Mocikat R., Pohlentz H.D.,				
RT	Zachau H.G.;				
RT	"Subgroup IV of human immunoglobulin K light chains is encoded by a				
RT	single germ-line gene."				
RL	Nucleic Acids Res. 13:6515-6529(1985).				
CC	-----				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: 200022; CAAT7317.1; -				
DR	PIR: A01904; K450J1.				
DR	HSSP: P01789; 2MCP.				
DR	INTERPRO: IPR003006; -				
DR	PFAM: PF00047; Ig: 1.				
KM	Immunoglobulin V region: Signal.				
FT	SIGNAL	21	133		
FT	CHAIN	1	20		
FT	DOMAIN	21	43		
FT	DOMAIN	44	75		
FT	DOMAIN	61	75		
FT	DOMAIN	76	82		
FT	DOMAIN	83	114		
FT	DOMAIN	115	122		
FT	DOMAIN	123	132		
FT	DISULFID	43	114		
FT	NON_TER	133	133		
SEQUENCE	133 AA: 14632 MW: 5FB3953066744AF4 CRC64:				

Query Match. 35.3%; Score 464; DB 1; Length 133;
Best local Similarity 75.0%; Pred. No. 1.2e-27;
Matches 87; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 134 GGGSDIELTQSPSSLAIVSGEYVANSCKSSQSLFNSRFRKNTLANTYQKPGGSPKYLTIW 193
DB 17 GAYGDIWMTQSPDSLAIVSGERATINCKSSQSVLSSNNKNTLANTYQKPGGPILLTIW 76

OY 194 ASTREGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCKOSYNLPFGGGTKLEIK 249
 DB 77 ASTREGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCKOQYDTPFGGGTKVEIK 132

RESULT 2

KV4C_HUMAN STANDARD; PRT; 134 AA.

AC P06314;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-86041854; PubMed-2997713;
 RA Marsh P., Mills F., Gould R.;
 RT "Detection of a unique human V kappa IV germline gene by a cloned
 RT cDNA probe."
 RL Nucleic Acids Res. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.

RA Submitted (OCT-1986) to the EMBL/Genbank/DBJ databases.

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DR EMBL: X02990; CA26733.1; -
 DR PIR: A01905; K4H017.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFM: PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 133 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 134 134
 SO SEQUENCE 134 AA; 14966 MW; 6413A22F0738832 CRC64;

Query Match 35.2%; Score 463.5; DB 1; Length 134;
 Best Local Similarity 76.1%; Pred. No. 1.3e+27;
 Matches 89; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

OY 134 GGSQDIETLQSPSSSLAVSAGEKYAMCKSSQSLFNSRTKNTIATYQKPGSPKLIYW 193
 DB 17 GAYGDIVMTQSPSLAVSLGERATINCKSSQSLVSSDNKNYLAWYQKPGPPKLIYW 76
 OY 194 ASTREGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCKOSYNLP-TFGGGTKLEIK 249
 DB 77 ASTREGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCOQYDTPFGGGTKVEIK 133

RESULT 3
 KV4A_HUMAN STANDARD; PRT; 114 AA.
 AC P01625;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION LEN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]

RP SEQUENCE.
 RX MEDLINE-76004342; PubMed-50995;
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of
 RT subgroup IV of the kappa type (Bence-Jones protein Len).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RN [2]
 RP REVISION TO 9.

RA Salomon A.;
 RL Submitted (AUG-1996) to the SWISS-PROT data bank.
 CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01903; K4H01N.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFM: PF00047; 19; 1.

KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 41 55 FRAMEWORK 2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 63 94 FRAMEWORK 3.
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 102 113 FRAMEWORK 4.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON_TER 114 114
 SO SEQUENCE 114 AA; 12640 MW; 0647F1D1FE236485 CRC64;

Query Match 34.1%; Score 448.5; DB 1; Length 114;
 Best Local Similarity 76.1%; Pred. No. 1.4e+26;
 Matches 86; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

OY 138 DIELQSPSSSLAVSAGEKYAMCKSSQSLFNSRTKNTIATYQKPGSPKLIYMASTR 197
 DB 1 DILVMTQSPSLAVSLGERATINCKSSQSLVSSDNKNYLAWYQKPGPPKLIYMASTR 60
 OY 198 ESGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCKOSYNLP-TFGGGTKLEIK 249
 DB 61 ESGVDPDRFTSGSGGDTFTLTSSVQAEDLAVYYCOQYDTPFGGGTKLEIK 113

RESULT 4
 KV4O_HUMAN STANDARD; PRT; 121 AA.
 AC P06312;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-86041853; PubMed-2997712;
 RA Klobbeck H.G., Bornkamm G.W., Combiato G., Moeckel R., Pohlenz H.D.,
 RA Zechau H.G.;
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
 RT single germline gene."
 RL Nucleic Acids Res. 13:6515-6529(1985).
 CC -I- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
 CC -----
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CC EMBL; 200023; CAA77318.1; -

DR PIR; A01902; K4HU.

DR HSSP; P01789; 2MCP.

DR INTERPRO; IPRO03006; -

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT CHAIN 1 20 IG KAPPA CHAIN V-IV REGION.

FT DOMAIN 21 >121 FRAMEWORK 1.

FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 61 75 FRAMEWORK 2.

FT DOMAIN 61 75 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 83 114 FRAMEWORK 3.

FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 43 114 BY SIMILARITY.

FT NON_TER 121 121

SO SEQUENCE 121 AA; 13380 MW; 9586AD418BD33974 CRC64;

Query Match 31.8%; Score 418; DB 1; Length 121;

Best Local Similarity 74.3%; Pred. No. 2.5e-24;

Matches 78; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 134 GGGSDIELTQSPSSSLAVSAGEKVAQSCSKSSQSLFNRRTNRYLAWYQKPGSPKLYIY 193

DB 17 GAYGDIVMTQSPDLSALVGERATINCKSSQSYLSNKNRYLAWYQKPGSPKLYIY 76

QY 194 ASTRESGVPRFTGSGSGTFTLTISVQAEADLVAVYCKNSYNLP 238

DB 77 ASTRESGVPRFTGSGSGTFTLTISVQAEADLVAVYCKNSYNLP 121

RESULT 5

HV07_MOUSE STANDARD; PRT; 139 AA.

ID P01751; P01752;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6;

RA MEDLINE-81234548; PubMed-6788376;

RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,

Baltimore D.;

RT "Heavy chain variable region contribution to the NPB family of

antibodies: somatic mutation evident in a gamma 2a variable region.,"

Cell 24:625-637(1981).

CC -I- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA

CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL

CC (NPB ANTIBODIES).

CC -----

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CC or send an email to license@isb-sib.ch).

CC EMBL; J00529; AAA38170.1; -

DR PIR; A02034; MEMS18.

DR INTERPRO; IPRO03006; -

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT CHAIN 1 19 IG HEAVY CHAIN V REGION B1-8/186-2.

FT DOMAIN 20 49 FRAMEWORK 1.

FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 50 54 FRAMEWORK 2.

FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 69 85 FRAMEWORK 3.

FT DOMAIN 86 117 D SEGMENT.

FT DOMAIN 118 124 D SEGMENT.

FT DOMAIN 125 139 JH2 SEGMENT.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 139 139

SO SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 30.4%; Score 400; DB 1; Length 139;

Best Local Similarity 63.4%; Pred. No. 6e-23;

Matches 78; Conservative 14; Mismatches 27; Indels 4; Gaps 2;

QY 1 OVRLQSGAEIVYSGASVNLSCASGFENIKDYMHVVKRPGEGLEMGIDPESEGETEY 60

DB 20 QVQLQPGAEIVKPGASVNLSCASGYTFTSYMHVVKRPGEGLEMGIDPNSSGTY 79

QY 61 APNFGKATVTDTSNTAVLHLSTSEDTTYVCNAVYYEYDGYA-LDYWGQGTIVY 119

DB 80 NEFKSKATLVNKPSTAVYMOVLSTLSDSAVYC---ARYVYSSYFDYWGQGTITL 136

QY 120 VSS 122

DB 137 VSS 139

RESULT 6

KVLA_MOUSE STANDARD; PRT; 114 AA.

ID P01632;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-I REGION S107A.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-81241357; PubMed-6788890;

RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;

RT "Nucleic acid and protein sequences of phosphocholine-binding light

chains.,"

J. Exp. Med. 153:1366-1370(1981).

CC -----

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CC EMBL; U29423; AAC00033.1; -

DR PIR; A01915; KVM57A.

DR HSSP; P01789; 2MCP.

DR INTERPRO; IPRO03006; -

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region.

FT CHAIN 1 23 FRAMEWORK 1.

FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 41 55 FRAMEWORK 2.

FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 63 94 FRAMEWORK 3.

FT DOMAIN 95 103 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 104 113 FRAMEWORK 4.


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ID KV5B_MOUSE STANDARD; PRT; 136 AA.
AC P01634;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG KAPPA CHAIN V-V REGION MOPC 21 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
and the diexonucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [2]
RP SEQUENCE OF 30-136.
RX MEDLINE=73053310; PubMed=4638343;
RA Swasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
CC -----
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CC -----
DR EMBL; V00810; CAA24192.1; ALT_TERM.
DR PIR; A01917; KYMS21.
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 29
FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.
FT DOMAIN 30 52 FRAMEWORK 1.
FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 64 78 FRAMEWORK 2.
FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 127 136 FRAMEWORK 4.
FT NON_TER 136
SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

Query Match 28.8%; Score 378.5; DB 1; Length 136;
Best Local Similarity 63.2%; Pred. No. 2.2e-21;
Matches 74; Conservative 18; Mismatches 18; Indels 7; Gaps 2;

QY 134 GGGSDILTSPSSILAVSAGEKVMKSCSQSLFNSRTKRYNYLAWYQKRGSGKVLIV 193
DB 26 GAGNIVMTQSPKSMVSGEYRLTLCKASENV-----TYSWYQKRPESKILIVG 79

QY 194 ASTRESGVPRFTGSGGSDFTLTISVQAEDLAIVYCKKSYNLP-TFGGKTLEIK 249
DB 80 ASNRKTVGPDRFTGSGGSDFTLTISVQAEDLADYHCGGYSYPTFGGKTLEIK 136

RESULT 10
HVL1_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
DR EMBL; J00539; AAA38172.1;
DR PIR; A02038; G2MS43.
DR INTERPRO; IPR003006;
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 FRAMEWORK 4.
FT DOMAIN 118 132 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8BC9 CRC64;

Query Match 28.7%; Score 378; DB 1; Length 137;
Best Local Similarity 61.5%; Pred. No. 2.4e-21;
Matches 75; Conservative 11; Mismatches 32; Indels 4; Gaps 2;

QY 1 OVKLOSAGELVSGASVYNSCTASGFNIRKDYMHVWKPREGSLWIGIDPESGETTV 60
DB 20 QVLDQPGAEVPGASVSKSCASGTTFTSYLHMVWNPGRGLEIGIDNSGCTTV 79

QY 61 APNFGKATVYADTSNTAVILHLSLTSEDTVYVCNAVIVYEDGYALDYGQGTTVV 120
DB 80 NEHFRSKATITIDKPSSTAVMQLSSLSDESAVYVC---ARYNLGRY-PDYWGQGTTLIV 135

QY 121 SS 122
DB 136 SS 137

RESULT 11
HVL2_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82152813; PubMed=6801765;
RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;

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"Somatic mutation in genes for the variable portion of the
RT Immunoglobulin heavy chain."
Science 216:309-311(1982).

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CC EMBL: J00493; AAA38128.1; -
DR PIR: A02028; HVM5G7.
DR INTERPRO: IPR003006; -
DR PIR: P000047; 19; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25AACBBE31DA5CE8 CRC64;

Query Match 28.6%; Score 376.5; DB 1; Length 140;
Best Local Similarity 58.2%; Pred. No. 3.1e-21;
Matches 71; Conservative 19; Mismatches 31; Indels 1; Gaps 1;

OY 1 OVLOESGAEIVRSGASVNLSCATSGFNKIDYIMHWKORPEGLMIGYIDPESGETEY 60
DB 20 EVLOQSGAEIVRSGASVNLSCATSGFNKIDYIMHWKORPEGLMIGYIDPESGETEY 79
OY 61 APNFOGKATVADTSSNTAYLHLSSLTSEDTYYCNAVYYEYEDGALDYMGOGTTVTV 120
DB 80 NEKKKGTTLTVDKSSSTAVWQLRLSLSEDSAYVFCARSHYGCSDPDPWGGTTLTV 138

OY 121 SS 122
DB 139 SS 140

RESULT 12
HVOI_MOUSE
ID HVOI_MOUSE STANDARD: PRT; 121 AA.
AC P01745;

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-81053741; PubMed-6253904;
RA Zakut R., Cohen J., Givol D.;
RT Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11."
RL Nucleic Acids Res. 8:3591-3601(1980).

RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR INTERPRO: IPR003006; -
DR PIR: A02027; GYMS11.

DR INTERPRO: IPR003006; -
DR PIR: P00047; 19; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 28.6%; Score 375.5; DB 1; Length 121;

Best Local Similarity 59.0%; Pred. No. 3.2e-21;
Matches 72; Conservative 18; Mismatches 31; Indels 1; Gaps 1;

OY 1 OVLOESGAEIVRSGASVNLSCATSGFNKIDYIMHWKORPEGLMIGYIDPESGETEY 60
DB 1 EVLOQSGAEIVRSGASVNLSCATSGFNKIDYIMHWKORPEGLMIGYIDPESGETEY 60
OY 61 APNFOGKATVADTSSNTAYLHLSSLTSEDTYYCNAVYYEYEDGALDYMGOGTTVTV 120
DB 61 NDNLKKGATLTADTSSNTAYLHLSSLTSEDTYYCNAVYYEYEDGALDYMGOGTTVTV 119

OY 121 SS 122
DB 120 SS 121

RESULT 13
KVLM_HUMAN
ID KVLM_HUMAN STANDARD: PRT; 129 AA.
AC P04431;

DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-85014148; PubMed-6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).

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CC EMBL: X00965; CAA25477.1; ALU_TERM.
DR PIR: A01883; KIH0WK.
DR HSSP: P01607; 1REI.
DR INTERPRO: IPR003006; -
DR PIR: P00047; 19; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 28.3%; Score 371.5; DB 1; Length 129;
Best Local Similarity 62.4%; Pred. No. 6.6e-21;
Matches 73; Conservative 20; Mismatches 17; Indels 7; Gaps 2;

OY 134 GGGSDIELTQSPSSSLAVSAGEKVMKSSQSLFNSRTKKNYLAWYQKPGSKVLYTV 193
DB 19 GARCIDQMOSPPSSLSASVGDRTITCRASQSI-----SNTLNMWQKPKAKPLIYA 72

OY 194 ASTRESGVDPFTGSGSGDTFTLTSSVOAEDLAVYYCKQSTN-LPTFGCGTKLEIK 249
DB 194 ASTRESGVDPFTGSGSGDTFTLTSSVOAEDLAVYYCKQSTN-LPTFGCGTKLEIK 249

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DB 73 ASSLSGVTNRFGSGSGDTFTLTITSSLOPEDSATYTCQGSYSTLTTFGGTRLEIK 129
RESULT 14
KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP MEDLINE-77038198; PubMed-824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scard J. Immunol. 5:677-684(1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; KIHUX.
DR HSSP: P01607; 1REL.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 2 34
FT DOMAIN 3 49
FT DOMAIN 4 56
FT DOMAIN 5 57
FT DOMAIN 6 88
FT DOMAIN 7 89
FT DOMAIN 8 97
FT DOMAIN 9 107
FT DISULFID 23
FT NON_TER 88
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 28.1%; Score 369.5; DB 1; Length 108;
Best Local Similarity 62.8%; Pred. No. 7.6e-21;
Matches 71; Conservative 20; Mismatches 15; Indels 7; Gaps 2;

QY 138 DIETQSPSSSLAVSAGEKVMKSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 197
DIQMTPSSSLASVGDRTVITCRASQNV-----NAYLNMWYQKPGKLRLIYGASTR 54
DB 1 198 ESGVPRFTGSGSGDTFTLTITSSVQAEADLAVYCKOSYNL-PTFGGTRLEIK 249
ESGVPRFTGSGSGDTFTLTITSSVQAEADLAVYCKOSYNL-PTFGGTRLEIK 249
DB 55 EAGVPRFTGSGSGDTFTLTITSSVQAEADLAVYCKOSYNL-PTFGGTRLEIK 107

RESULT 15
KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP MEDLINE-71032830; PubMed-4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
```

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RT chain of subgroup I (Bence-Jones Protein HAU): subdivision within
RT subgroups."
RT Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01868; KIHOU.
DR HSSP: P80362; 1MTL.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 2 34
FT DOMAIN 3 49
FT DOMAIN 4 56
FT DOMAIN 5 57
FT DOMAIN 6 88
FT DOMAIN 7 89
FT DOMAIN 8 97
FT DOMAIN 9 107
FT DISULFID 23
FT NON_TER 88
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 27.9%; Score 367.5; DB 1; Length 108;
Best Local Similarity 61.9%; Pred. No. 1.1e-20;
Matches 70; Conservative 22; Mismatches 14; Indels 7; Gaps 2;

QY 138 DIETQSPSSSLAVSAGEKVMKSSQSLFNSRTRKNTLAWYQKPGQSPKVLIIYMASTR 197
DIQMTPSSSLASVGDRTVITCRASQNV-----SSYLSWYQKPGKAPQVLIYMASSL 54
DB 1 198 ESGVPRFTGSGSGDTFTLTITSSVQAEADLAVYCKOSYNL-PTFGGTRLEIK 249
ESGVPRFTGSGSGDTFTLTITSSVQAEADLAVYCKOSYNL-PTFGGTRLEIK 249
DB 55 EAGVPRFTGSGSGDTFTLTITSSVQAEADLAVYCKOSYNL-PTFGGTRLEIK 107
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Search completed: February 12, 2001, 15:26:39
Job time: 195 sec

